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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 23:15:04 ; Search time 443 Seconds
(without alignments)
10105.763 Million cell updates/sec

Title: US-10-798-721-9
Perfect score: 2736
Sequence: 1 atggggagagcggcggccac.....gcaggcaaaatggactctag 2736

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2736	100.0	2736	4	US-09-969-532-9	Sequence 9, Appli
	2	2736	100.0	3411	4	US-09-969-532-33	Sequence 33, Appl
	3	2660	97.2	2703	4	US-09-969-532-11	Sequence 11, Appl
	4	2642	96.6	2694	4	US-09-969-532-13	Sequence 13, Appl
	5	2566	93.8	2661	4	US-09-969-532-15	Sequence 15, Appl
	6	2043	74.7	2043	4	US-09-969-532-25	Sequence 25, Appl
	7	1967	71.9	2010	4	US-09-969-532-27	Sequence 27, Appl
	8	1949	71.2	2001	4	US-09-969-532-29	Sequence 29, Appl
	9	1873	68.5	1968	4	US-09-969-532-31	Sequence 31, Appl
	10	1640	59.9	1734	4	US-09-969-532-1	Sequence 1, Appli
	11	1564	57.2	1701	4	US-09-969-532-3	Sequence 3, Appli
	12	1546	56.5	1692	4	US-09-969-532-5	Sequence 5, Appli
	13	1470	53.7	1659	4	US-09-969-532-7	Sequence 7, Appli
	14	947	34.6	1041	4	US-09-969-532-17	Sequence 17, Appl
	15	871	31.8	1008	4	US-09-969-532-19	Sequence 19, Appl
	16	853	31.2	999	4	US-09-969-532-21	Sequence 21, Appl
	17	777	28.4	966	4	US-09-969-532-23	Sequence 23, Appl
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	19	544	19.9	2831	3	US-09-306-902A-3	Sequence 3, Appli
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	21	487	17.8	3014	3	US-09-306-902A-1	Sequence 1, Appli
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c	33	49.6	1.8	601	4	US-09-949-016-170041	Sequence 170041,
c	34	47	1.7	601	4	US-09-949-016-170000	Sequence 170000,
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	36	42.4	1.5	4548	4	US-09-571-479C-5	Sequence 5, Appli
c	37	42.2	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
c	38	40	1.5	601	4	US-09-949-016-170034	Sequence 170034,
	39	39.8	1.5	75929	4	US-09-949-016-15543	Sequence 15543, A
	40	39.8	1.5	75929	4	US-09-949-016-15544	Sequence 15544, A
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	43	39	1.4	1507	4	US-09-270-767-16560	Sequence 16560, A
	44	38	1.4	1141	4	US-09-806-708B-22	Sequence 22, Appl
	45	37.8	1.4	7218	1	US-08-232-463-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-969-532-9
; Sequence 9, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-9

Query Match 100.0%; Score 2736; DB 4; Length 2736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 33, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 3411
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-33

  Query Match           100.0%;  Score 2736;  DB 4;  Length 3411;
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  Matches 2736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1255 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1314

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
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Db       1315 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1374

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1375 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1434

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
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Db       1435 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1494

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1495 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1554

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1614

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1674

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1734
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Qy      1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
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Db      1735 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1794

Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1795 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1854

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1855 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1914

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1915 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1974

Qy      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1975 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 2034

Qy      1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2035 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 2094

Qy      1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2095 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2154

Qy      2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2155 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2214

Qy      2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2215 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2274

Qy      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2275 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2334

Qy      2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2335 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2394

Qy      2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2395 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2454

Qy      2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2455 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2514

Qy      2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2515 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2574

Qy      2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2575 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2634

Qy      2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2635 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2694

Qy      2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2695 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2754

Qy      2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2755 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2814

Qy      2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db      2815 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2850
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RESULT 3
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Query Match 97.2%; Score 2660; DB 4; Length 2703;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy         1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy        61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
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Db       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Db       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
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Qy       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
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Qy       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Db       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
Db       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Db       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy       901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
Db       901 GGTCTTTGCATCCTAG----------------------------------GCATTGAGAAT 927

Qy       961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db       928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db       988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047

Qy      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db       1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1107

Qy      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db       1108 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1167

Qy      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db       1168 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1227

Qy      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db       1228 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1287

Qy      1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
Db       1288 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1347

Qy      1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
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Qy      1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
Db       1408 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1467

Qy      1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
Db       1468 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1527

Qy      1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
Db       1528 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1587

Qy      1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
Db       1588 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1647

Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
Db       1648 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1707

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
Db       1708 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1767

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
Db       1768 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1827

Qy      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
Db       1828 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1887

Qy      1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
Db       1888 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1947

Qy      1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
Db       1948 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2007

Qy      2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
Db       2008 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2067

Qy      2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
Db       2068 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2127

Qy      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
Db       2128 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2187

Qy      2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
Db       2188 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2247

Qy      2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
Db       2248 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2307

Qy      2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
Db       2308 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2367

Qy      2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
Db       2368 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2427

Qy      2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
Db       2428 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2487

Qy      2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
Db       2488 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2547

Qy      2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
Db       2548 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2607

Qy      2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
Db       2608 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2667

Qy      2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
Db       2668 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2703
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RESULT 4
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232

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; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-13

  Query Match             96.6%;  Score 2642;  DB 4;  Length 2694;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 2694;  Conservative    0;  Mismatches    0;  Indels   42;  Gaps    1;

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Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1134

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1158

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1218

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1278

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1338

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1398

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1458

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1518

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1578

Qy       1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1638

Qy       1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1698

Qy       1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1758

Qy       1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1818

Qy       1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
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Db       1819 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1878

Qy       1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1938

Qy       1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 1998

Qy       2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2058

Qy       2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2118

Qy       2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2178

Qy       2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2238

Qy       2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2298

Qy       2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2299 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2358

Qy       2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2359 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2418

Qy       2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2478

Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2538

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2539 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2598

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2599 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2658

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db       2659 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2694


RESULT 5
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 2661
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-15

  Query Match            93.8%;  Score 2566;  DB 4;  Length 2661;
  Best Local Similarity  97.3%;  Pred. No. 0;
  Matches 2661;  Conservative    0;  Mismatches    0;  Indels   75;  Gaps    2;

Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
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Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
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Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
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Db        901 GGTCTTTGCATCCTAG------------------------------GCATTGAGAAT 927

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1101

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
                                                  ||||||||||||||||||||||||
Db       1102 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1125

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1185

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1245

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1305

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1365

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1425

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1485

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1545

Qy       1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1605

Qy       1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1606 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1665

Qy       1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1666 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1725

Qy       1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1785

Qy       1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1845

Qy       1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1905

Qy       1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1906 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 1965

Qy       2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2025

Qy       2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
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Db       2026 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2085

Qy       2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2145

Qy       2221 CGGCAGCCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 CGGCAGCCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2205

Qy       2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2265

Qy       2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2325

Qy       2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2385

Qy       2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2445

Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2505

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2565

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2625

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
              ||||||||||||||||||||||||||||||||||||
Db       2626 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2661
```

RESULT 6
US-09-969-532-25
; Sequence 25, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-25

Query Match 74.7%; Score 2043; DB 4; Length 2043;

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Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2043;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 240

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 420

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 480

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 540

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 600

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 660

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 720

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 780

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 840

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 900

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 960

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1020

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1080

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1140

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1200

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1260

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1320

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1380

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1440

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1500

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1560

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1620

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1680

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1740

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1800

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1860

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1920

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1980

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2040

Qy       2734 TAG 2736
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Db       2041 TAG 2043

RESULT 7
US-09-969-532-27
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; Sequence 27, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 2010
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-27

  Query Match           71.9%;  Score 1967;  DB 4;  Length 2010;
  Best Local Similarity  98.4%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG---------------- 223

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ----------------GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 267

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 327

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 387

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 447

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 507

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 567

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 627

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 687

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        688 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 747

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 807

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 867

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 927

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 987

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1047

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1107

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1167

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1227

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1287

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1347

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1407

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1467

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1527

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1587

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1647

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1707

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1767

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1827
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Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1828 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1887

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1947

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2007

Qy       2734 TAG 2736
              |||
Db       2008 TAG 2010


RESULT 8
US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 2001
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-29

  Query Match             71.2%;  Score 1949;  DB 4;  Length 2001;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 2001;  Conservative    0;  Mismatches    0;  Indels   42;  Gaps    1;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 240

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 420

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||||

Db        421 AACTTCAAAACAGTCCGTCAA---------------------------------------- 441

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ---GGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 498

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 558

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 618

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 678

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 738

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 798

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 858

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 918

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 978

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1038

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1039 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1098

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1099 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1158

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1159 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1218

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1219 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1278

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1279 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1338

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1339 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1398

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1399 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1458

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1459 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1518
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Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1578

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1638

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1698

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1758

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1818

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1878

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1938

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 1998

Qy       2734 TAG 2736
             |||
Db       1999 TAG 2001
```

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RESULT 9
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 1968
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-31

  Query Match            68.5%;  Score 1873;  DB 4;  Length 1968;
  Best Local Similarity  96.3%;  Pred. No. 0;
  Matches 1968;  Conservative    0;  Mismatches    0;  Indels   75;  Gaps    2;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG---------------- 223

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ----------------GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 267

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 327

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 387

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||
Db        388 AACTTCAAAACAGTCCGTCAA---------------------------------------- 408

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 ---GGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 465

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 525

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 585

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 645

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 705

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 765

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 825

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 885

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 945

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1005

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1065

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1125

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1185
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Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1245

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1305

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1365

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1425

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1485

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1545

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1605

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1606 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1665

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1666 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1725

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1726 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1785

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1786 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1845

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1905

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1906 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 1965

Qy       2734 TAG 2736
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Db       1966 TAG 1968
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RESULT 10
US-09-969-532-1
; Sequence 1, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/09/969,532
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 1
;   LENGTH: 1734
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-969-532-1

  Query Match             59.9%;  Score 1640;  DB 4;  Length 1734;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1640;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
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Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
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Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
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Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
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Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
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Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
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Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
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Db        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
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Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
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Db        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
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Db       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
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Db       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620

Qy       1621 ATCAACCAAGGTGAACCCAG 1640
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Db       1621 ATCAACCAAGGTGAACCCAG 1640
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RESULT 11
US-09-969-532-3
; Sequence 3, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-3

Query Match 57.2%; Score 1564; DB 4; Length 1701;
Best Local Similarity 98.0%; Pred. No. 0;

Matches 1607; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
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Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
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Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
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Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
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Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
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Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
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Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
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Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
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Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
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Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTCTTTGCATCCTAG----------GCATTGAGAAT 927

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
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Db        988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047
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Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
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Db       1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1107

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1167

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1227

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1287

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
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Db       1288 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1347

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
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Db       1348 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1407

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
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Db       1408 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1467

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
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Db       1468 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1527

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1587

Qy       1621 ATCAACCAAGGTGAACCCAG 1640
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Db       1588 ATCAACCAAGGTGAACCCAG 1607
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RESULT 12
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Query Match 56.5%; Score 1546; DB 4; Length 1692;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1598; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
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Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
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Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
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Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
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Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
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Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
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Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
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Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
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Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1134

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
                                                  ||||||||||||||||||||||||
Db       1135 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1158
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Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1218

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1278

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1338

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1398

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1458

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1518

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1578

Qy       1621 ATCAACCAAGGTGAACCCAG 1640
             ||||||||||||||||||||
Db       1579 ATCAACCAAGGTGAACCCAG 1598
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RESULT 13
US-09-969-532-7
; Sequence 7, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-7

Query Match 53.7%; Score 1470; DB 4; Length 1659;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 0; Indels 75; Gaps 2;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
              |||||||||||||||                                ||||||||||||
Db        901 GGTCTTTGCATCCTAG--------------------------------GCATTGAGAAT 927

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1101

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1125

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1185

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1245
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Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1305

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1365

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1425

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1485

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1545

Qy       1621 ATCAACCAAGGTGAACCCAG 1640
             ||||||||||||||||||||
Db       1546 ATCAACCAAGGTGAACCCAG 1565
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RESULT 14
US-09-969-532-17
; Sequence 17, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-17

Query Match 34.6%; Score 947; DB 4; Length 1041;
Best Local Similarity 100.0%; Pred. No. 1.3e-289;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 240

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 420

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 480

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 540

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 600

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 660

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 720

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 780

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 840

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 900

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG 1640
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG 947
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RESULT 15
US-09-969-532-19
; Sequence 19, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-19

Query Match 31.8%; Score 871; DB 4; Length 1008;
Best Local Similarity 96.5%; Pred. No. 1.8e-265;
Matches 914; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
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Db        61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy       814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy       874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
            ||||||||||||||||||||||||||||||||||||||||
Db       181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG---------------- 223

Qy       934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                          ||||||||||||||||||||||||||||||||||||||||||||||
Db       224 ----------------GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 267

Qy       994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 327

Qy      1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       328 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 387

Qy      1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       388 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 447

Qy      1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       448 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 507

Qy      1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       508 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 567

Qy      1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       568 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 627

Qy      1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       628 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 687

Qy      1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       688 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 747

Qy      1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       748 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 807

Qy      1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       808 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 867

Qy      1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG 1640
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Db       868 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG 914
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Search completed: April 1, 2005, 05:46:11
Job time : 467 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 23:37:48 ; Search time 1514 Seconds
(without alignments)
10937.661 Million cell updates/sec

Title: US-10-798-721-9
Perfect score: 2736
Sequence: 1 atggggagagcggcggccac.....gcaggcaaaatggactctag 2736

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2736	100.0	2736	18	US-10-798-721-9	Sequence 9, Appli
2	2736	100.0	3411	18	US-10-798-721-33	Sequence 33, Appl
3	2660	97.2	2703	18	US-10-798-721-11	Sequence 11, Appl
4	2642	96.6	2694	18	US-10-798-721-13	Sequence 13, Appl
5	2566	93.8	2661	18	US-10-798-721-15	Sequence 15, Appl
6	2320.8	84.8	8899	18	US-10-723-860-7444	Sequence 7444, Ap
7	2287	83.6	2979	18	US-10-473-518-136	Sequence 136, App
8	2284	83.5	2868	19	US-10-872-681-55	Sequence 55, Appl
9	2260	82.6	2898	17	US-10-094-886-115	Sequence 115, App
10	2220	81.1	2661	19	US-10-872-681-53	Sequence 53, Appl
11	2043	74.7	2043	18	US-10-798-721-25	Sequence 25, Appl
12	1967	71.9	2010	18	US-10-798-721-27	Sequence 27, Appl
13	1949	71.2	2001	18	US-10-798-721-29	Sequence 29, Appl
14	1873	68.5	1968	18	US-10-798-721-31	Sequence 31, Appl
15	1640	59.9	1734	18	US-10-798-721-1	Sequence 1, Appli
16	1564	57.2	1701	18	US-10-798-721-3	Sequence 3, Appli
17	1546	56.5	1692	18	US-10-798-721-5	Sequence 5, Appli
18	1470	53.7	1659	18	US-10-798-721-7	Sequence 7, Appli
19	947	34.6	1041	18	US-10-798-721-17	Sequence 17, Appl
20	871	31.8	1008	18	US-10-798-721-19	Sequence 19, Appl
21	867.8	31.7	2181	17	US-10-094-886-117	Sequence 117, App
22	853	31.2	999	18	US-10-798-721-21	Sequence 21, Appl
23	777	28.4	966	18	US-10-798-721-23	Sequence 23, Appl
24	597	21.8	2860	17	US-10-087-684-1	Sequence 1, Appli
25	597	21.8	2860	17	US-10-218-779-1	Sequence 1, Appli
26	592.2	21.6	2860	17	US-10-087-684-3	Sequence 3, Appli
27	592.2	21.6	2860	17	US-10-218-779-3	Sequence 3, Appli
28	590	21.6	3485	9	US-09-816-828-18	Sequence 18, Appl
29	588.6	21.5	3884	14	US-10-028-072-145	Sequence 145, App
30	588.6	21.5	3884	14	US-10-140-808-145	Sequence 145, App
31	588.6	21.5	3884	14	US-10-121-049-145	Sequence 145, App
32	588.6	21.5	3884	14	US-10-123-904-145	Sequence 145, App
33	588.6	21.5	3884	14	US-10-140-470-145	Sequence 145, App
34	588.6	21.5	3884	14	US-10-175-746-145	Sequence 145, App
35	588.6	21.5	3884	14	US-10-176-918-145	Sequence 145, App
36	588.6	21.5	3884	14	US-10-176-921-145	Sequence 145, App
37	588.6	21.5	3884	14	US-10-137-865-145	Sequence 145, App
38	588.6	21.5	3884	14	US-10-140-474-145	Sequence 145, App
39	588.6	21.5	3884	14	US-10-142-431-145	Sequence 145, App
40	588.6	21.5	3884	14	US-10-143-114-145	Sequence 145, App
41	588.6	21.5	3884	14	US-10-142-419-145	Sequence 145, App
42	588.6	21.5	3884	14	US-10-123-262-145	Sequence 145, App
43	588.6	21.5	3884	14	US-10-142-423-145	Sequence 145, App
44	588.6	21.5	3884	14	US-10-121-050-145	Sequence 145, App
45	588.6	21.5	3884	14	US-10-141-755-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-10-798-721-9
; Sequence 9, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-9

Query Match 100.0%; Score 2736; DB 18; Length 2736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
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Qy       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
Db       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
Db       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
Db       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
Db       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
Db       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
Db       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
Db       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Qy       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
Db       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
Db       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Db       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
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Qy       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
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Db       901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

Qy       961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
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Qy      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140

Qy      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200

Qy      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260

Qy      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320

Qy      1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
Db      1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380

Qy      1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
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Qy      1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
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Qy      1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
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Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACCATCCCGCAC 1740
Db      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACCATCCCGCAC 1740

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
Db      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
Db      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860

Qy      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
Db      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920

Qy      1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
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Qy      1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
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Qy      2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
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Qy      2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
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Qy      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
Db      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220

Qy      2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
Db      2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280

Qy      2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
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Db       2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340

Qy       2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400

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Db       2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460

Qy       2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520

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Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580

Db       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640

Db       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700

Db       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736

Db       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736


RESULT 2
US-10-798-721-33
; Sequence 33, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/10/798,721
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: US/09/969,532
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 3411
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-798-721-33

  Query Match             100.0%;  Score 2736;  DB 18;  Length 3411;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Db        175 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 234

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Db        235 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 294

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Db        295 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 354

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

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Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Db        475 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 534

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Db        535 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 594

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Db        595 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 654

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Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Db        715 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 774

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Db        775 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 834

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Db        835 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 894

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Db        895 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 954

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Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

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Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Db       1135 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1194

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140

Db       1195 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1254

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200

Db       1255 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1314

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260

Db       1315 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1374

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320

Db       1375 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1434
```

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Qy      1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1435 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1494

Qy      1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1495 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1554

Qy      1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1555 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1614

Qy      1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1615 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1674

Qy      1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1675 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1734

Qy      1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
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Db      1735 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1794

Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1795 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1854

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1855 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1914

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1915 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1974

Qy      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1975 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 2034

Qy      1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2035 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 2094

Qy      1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2095 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2154

Qy      2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2155 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2214

Qy      2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2215 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2274

Qy      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2275 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2334

Qy      2221 CGGCAGCCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2335 CGGCAGCCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2394

Qy      2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2395 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2454

Qy      2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2455 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2514

Qy      2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2515 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2574

Qy      2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2575 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2634

Qy      2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2635 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2694

Qy      2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2695 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2754

Qy      2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2755 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2814

Qy      2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db      2815 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2850
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RESULT 3
US-10-798-721-11
; Sequence 11, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-11

Query Match 97.2%; Score 2660; DB 18; Length 2703;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy        61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
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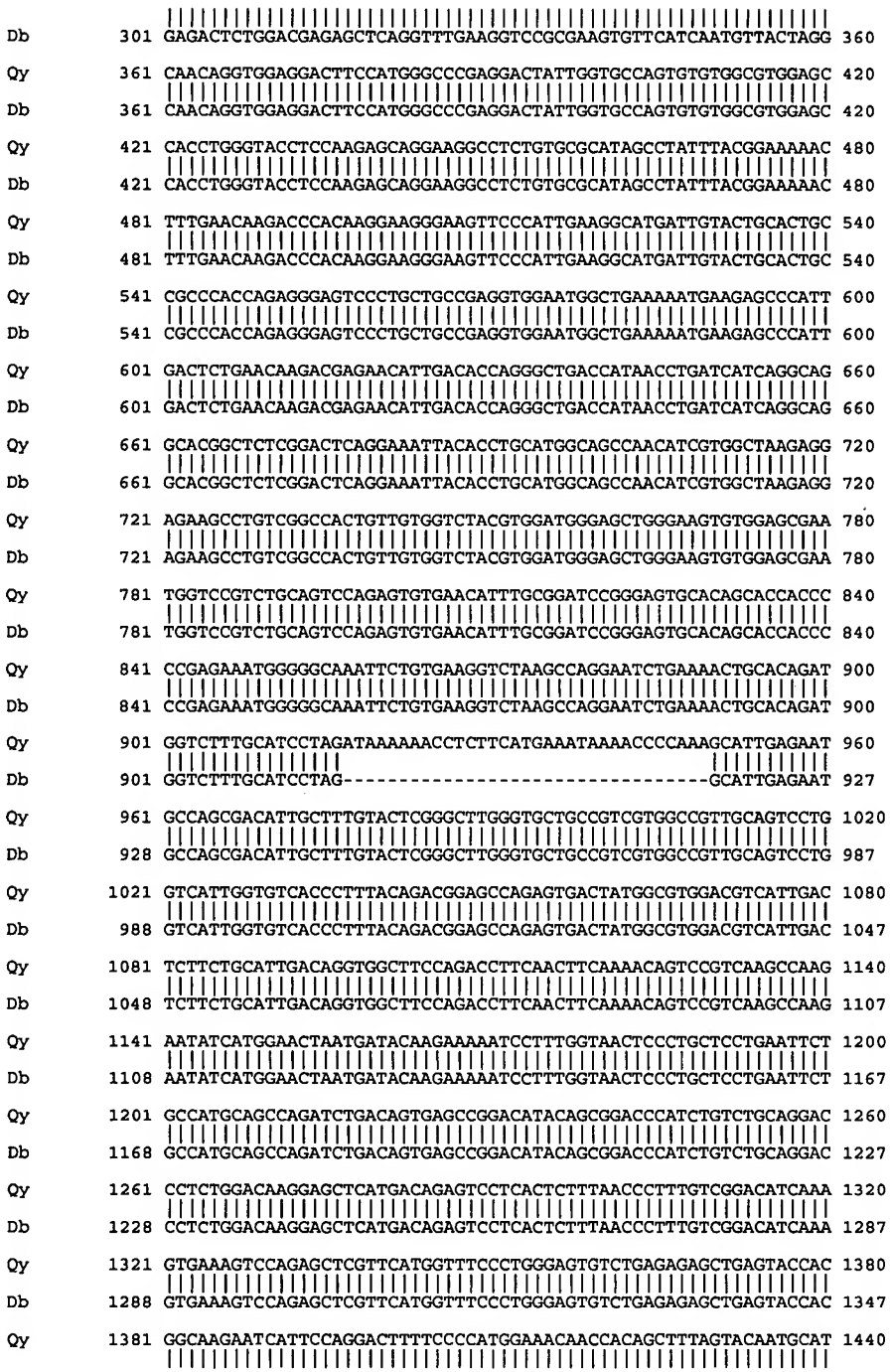
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Qy 361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
Db 361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
Qy 421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Qy 481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Qy 541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
Db 541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Db 601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
Qy 661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
Db 661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
Qy 721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Db 721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Qy 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
Db 781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
Qy 841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Db 841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Qy 901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
Db 901 GGTCTTTGCATCCTAG----------GCATTGAGAAT 927
Qy 961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db 928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987
Qy 1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db 988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047
Qy 1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db 1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1107
Qy 1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db 1108 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1167
Qy 1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db 1168 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1227
Qy 1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db 1228 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1287
Qy 1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
Db 1288 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1347
Qy 1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
Db 1348 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1407
Qy 1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
Db 1408 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1467
Qy 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
Db 1468 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1527
Qy 1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
Db 1528 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1587
Qy 1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
Db 1588 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1647
Qy 1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
Db 1648 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1707
Qy 1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
Db 1708 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1767
Qy 1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
Db 1768 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1827
Qy 1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
Db 1828 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1887
Qy 1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
Db 1888 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1947
Qy 1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
Db 1948 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2007
Qy 2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
Db 2008 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2067
Qy 2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
Db 2068 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2127
Qy 2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
Db 2128 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2187
Qy 2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
Db 2188 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2247
Qy 2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
Db 2248 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2307
Qy 2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
Db 2308 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2367
Qy 2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
Db 2368 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2427
Qy 2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
Db 2428 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2487

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Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
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Db       2488 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2547

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2548 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2607

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
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Db       2608 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2667

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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RESULT 4
US-10-798-721-13
; Sequence 13, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/10/798,721
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: US/09/969,532
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 2694
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-798-721-13

  Query Match             96.6%;  Score 2642;  DB 18;  Length 2694;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 2694;  Conservative    0;  Mismatches    0;  Indels   42;  Gaps    1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
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Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Qy        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
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Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1134

Qy       1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1158

Qy       1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1218

Qy       1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1278

Qy       1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1338

Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1398

Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1458

Qy       1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
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Db       1459 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1518

Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1578

Qy       1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1638

Qy       1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1698

Qy       1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1758

Qy       1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1818

Qy       1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1878

Qy       1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1938

Qy       1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 1998

Qy       2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
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Db       1999 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2058

Qy       2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2118

Qy       2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2178

Qy       2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2238

Qy       2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2298

Qy       2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2299 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2358

Qy       2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2359 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2418

Qy       2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2478

Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2538

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2539 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2598

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2599 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2658

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
             |||||||||||||||||||||||||||||||||||
Db       2659 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2694
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RESULT 5
US-10-798-721-15
; Sequence 15, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-15

Query Match 93.8%; Score 2566; DB 18; Length 2661;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 75; Gaps 2;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Qy       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
Db       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
Db       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
Db       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Db       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
Db       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Db       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy       901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
Db       901 GGTCTTTGCATCCTAG----------------------------------GCATTGAGAAT 927

Qy       961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db       928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db       988 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1047

Qy      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db       1048 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA------ 1101

Qy      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db       1102 ----------------------------------GGTAACTCCCTGCTCCTGAATTCT 1125

Qy      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db       1126 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1185

Qy      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db       1186 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1245

Qy      1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
Db       1246 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1305

Qy      1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
Db       1306 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1365

Qy      1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
Db       1366 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1425

Qy      1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
Db       1426 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1485

Qy      1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
Db       1486 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1545

Qy      1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
Db       1546 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1605

Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
Db       1606 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1665

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
Db       1666 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1725

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
Db       1726 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1785

Qy      1861 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1920
Db       1786 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 1845

Qy      1921 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1980
Db       1846 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 1905

Qy      1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
Db       1906 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 1965

Qy      2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
Db       1966 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2025

Qy      2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
Db       2026 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2085

Qy      2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
Db       2086 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2145

Qy      2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
Db       2146 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2205

Qy      2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
Db       2206 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2265

Qy      2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
Db       2266 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2325

Qy      2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
Db       2326 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2385

Qy      2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
Db       2386 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2445

Qy      2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
Db       2446 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2505

Qy      2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
Db       2506 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2565

Qy      2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
Db       2566 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2625

Qy      2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db       2626 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2661


RESULT 6
US-10-723-860-7444
; Sequence 7444, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7444
;   LENGTH: 8899
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (133)..(167)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2173)..(2189)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2947)..(2972)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5055)..(5069)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (7333)..(7350)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-7444

  Query Match            84.8%;  Score 2320.8;  DB 18;  Length 8899;
  Best Local Similarity  90.6%;  Pred. No. 0;
  Matches 2552;  Conservative    0;  Mismatches   54;  Indels  210;  Gaps    2;

Qy         89 CCGCGGCTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTC 148
              ||                                  ||||||||||||||||||||||
Db        129 CCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCGAATCCATCCCATCAGCTC 188

Qy        149 CTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACC 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACC 248

Qy        209 CTATTGCACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCG 268
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Db        249 CTATTGCACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCG 308

Qy        269 AGTGGGTCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGA 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 AGTGGGTCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGA 368

Qy        329 AGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 388
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Db        369 AGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 428

Qy        389 AGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGG 448
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Db        429 AGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGG 488

Qy        449 CCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAG 508
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Db        489 CCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAG 548

Qy        509 TTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCG 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 TTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCG 608

Qy        569 AGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACA 628
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Db        609 AGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACA 668

Qy        629 CCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACA 688
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Db        669 CCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACA 728

Qy        689 CCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCT 748
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Db        729 CCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCT 788

Qy        749 AC---------------------------------------------------------- 750
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Db        789 ACGTGAATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTA 848

Qy        751 ---------------------------------------------------------- 750

Db        849 GAGGATGGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCT 908

Qy        751 ----------------------------------------------------GTGGATGGGA 760
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Db        909 TTTGTGAGGGAATGTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGA 968

Qy        761 GCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCC 820
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Db        969 GCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCC 1028

Qy        821 GGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGG 880
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Db       1029 GGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGG 1088

Qy        881 AATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAA 940
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Db       1089 AATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAA 1148

Qy        941 AACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCG 1000
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Db       1149 AACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCG 1208

Qy       1001 TCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACT 1060
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Qy       1061 ATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCA 1120
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Db       1269 ATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCA 1328

Qy       1121 AAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTA 1180
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Db       1329 AAACAGTCCGTCAA----------------------------------------GGTA 1346

Qy       1181 ACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCG 1240
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Db       1347 ACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCG 1406

Qy       1241 GACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTA 1300
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Db       1407 GACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTA 1466

Qy       1301 ACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGT 1360
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Db       1467 ACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGT 1526
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Qy       1361 CTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACC 1420
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Db       1527 CTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACC 1586

Qy       1421 ACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1480
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Db       1587 ACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1646

Qy       1481 TCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1540
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Db       1647 TCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1706

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Db       1707 TAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATT 1766

Qy       1601 CTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTG 1660
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Db       1767 CTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTG 1826

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Qy       1721 TTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAA 1780
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Db       1887 TTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAA 1946

Qy       1781 AGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACAT 1840
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Db       2067 ATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTT 2126

Qy       1961 TTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATA 2020
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Qy       2021 CCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGG 2080
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Db       2187 NNNCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGG 2246

Qy       2081 AAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTG 2140
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Db       2247 AAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTG 2306

Qy       2141 ATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCT 2200
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Qy       2201 CCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATA 2260
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Qy       2261 CGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAAC 2320
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Db       2427 CGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAAC 2486

Qy       2321 AGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCG 2380
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Db       2487 AGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCG 2546

Qy       2381 CACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACT 2440
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Db       2547 CACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACT 2606

Qy       2441 CCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGC 2500
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Db       2607 CCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGC 2666

Qy       2501 AGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTA 2560
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Db       2667 AGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTA 2726

Qy       2561 GCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTG 2620
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Db       2727 GCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTG 2786

Qy       2621 ACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTT 2680
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Db       2787 ACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTT 2846

Qy       2681 CAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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RESULT 7
US-10-473-518-136
; Sequence 136, Application US/10473518
; Publication No. US20040138416A1
; GENERAL INFORMATION:
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; APPLICANT: LEE, Ernestine A.
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; APPLICANT: BOROWSKY, Mark L.
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; APPLICANT: GRAUL, Richard C.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PF-0933 USN
; CURRENT APPLICATION NUMBER: US/10/473,518
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/US02/09923
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; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/285,336
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/283,714
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/280,683
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PERL Program
; SEQ ID NO 136
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7289994CB1
US-10-473-518-136

Query Match 83.6%; Score 2287; DB 18; Length 2979;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2560; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

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Qy       102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161
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Db       213 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 272

Qy       162 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 221
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Qy       402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 461
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Qy       462 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 521
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Qy       582 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 641
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Qy       642 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 701
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Qy       702 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---------- 750
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Qy       751 ---------------------------------------------------------- 750

Db       873 CTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAGAA 932

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Qy       751 ----------------------------------GTGGATGGGAGCTGGGAAGTGTG 773
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Db       993 GTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 1052

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Db      1053 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 1112

Qy       834 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 893
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Db      1113 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 1172

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Db      1173 CACAGATGGTCTTTGCATCCTAG--------------------------------GCAT 1199

Qy       954 TGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGC 1013
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Db      1200 TGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGC 1259

Qy      1014 AGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGT 1073
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Db      1260 AGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGT 1319

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Qy      1134 AGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCT 1193
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Db      1458 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGA 1517

Qy      1314 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1373
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Db      1518 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1577

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Qy      1434 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 1493
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Db      1818 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 1877

Qy      1674 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 1733
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1878 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 1937

Qy      1734 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1793
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1938 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1997

Qy      1794 GCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCT 1853
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1998 GCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCT 2057

Qy      1854 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 1913
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2058 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 2117

Qy      1914 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 1973
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2118 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 2177

Qy      1974 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2033
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Db       2178 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2237

Qy       2034 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2093

Db       2238 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2297

Qy       2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2153

Db       2298 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2357

Qy       2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213

Db       2358 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2417

Qy       2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273

Db       2418 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2477

Qy       2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333

Db       2478 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2537

Qy       2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393

Db       2538 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2597

Qy       2394 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2453

Db       2598 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2657

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Db       2658 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2717

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Qy       2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633

Db       2778 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2837

Qy       2634 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2693

Db       2838 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2897

Qy       2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736

Db       2898 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2940
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RESULT 8
US-10-872-681-55
; Sequence 55, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
;  APPLICANT: ARES TRADING LIMITED
;  TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
;  FILE REFERENCE: P029209WO
;  CURRENT APPLICATION NUMBER: US/10/872,681
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: GB0130721.4
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 55
;   LENGTH: 2868
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SEQ ID NO:33
US-10-872-681-55
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Query Match 83.5%; Score 2284; DB 19; Length 2868;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2557; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

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Qy        102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161

Db        144 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 203

Qy        162 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 221

Db        204 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 263

Qy        222 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 281

Db        264 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 323

Qy        282 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 341

Db        324 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 383

Qy        342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 401

Db        384 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 443

Qy        402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 461

Db        444 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 503

Qy        462 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 521

Db        504 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 563

Qy        522 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 581

Db        564 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 623

Qy        582 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 641

Db        624 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 683

Qy        642 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 701

Db        684 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 743

Qy        702 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---------- 750

Db        744 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGAATGGAGG 803

Qy        751 ---------------------------------------------------------- 750

Db        804 CTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAGAA 863

Qy        751 ---------------------------------------------------------- 750

Db        864 ACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTGAGGGAAT 923

Qy        751 ----------------------------------GTGGATGGGAGCTGGGAAGTGTG 773

Db        924 GTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 983

Qy        774 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 833

Db        984 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 1043

Qy        834 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 893

Db       1044 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 1103

Qy        894 CACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCAT 953

Db       1104 CACAGATGGTCTTTGCATCCTAG--------------------------------GCAT 1130
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Qy       954 TGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGC 1013
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1131 TGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGC 1190

Qy      1014 AGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGT 1073
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1191 AGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGT 1250

Qy      1074 CATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCA 1133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1251 CATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCA 1310

Qy      1134 AGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCT 1193
            |                                          ||||||||||||||||||
Db      1311 A------------------------------------------GGTAACTCCCTGCTCCT 1328

Qy      1194 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1253
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Db      1329 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1388

Qy      1254 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGA 1313
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Db      1389 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGA 1448

Qy      1314 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1373
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1449 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1508

Qy      1374 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 1433
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1509 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 1568

Qy      1434 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 1493
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1569 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 1628

Qy      1494 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATAC 1553
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1629 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATAC 1688

Qy      1554 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 1613
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1689 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 1748

Qy      1614 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 1673
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1749 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 1808

Qy      1674 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 1733
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1809 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 1868

Qy      1734 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1793
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1869 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1928

Qy      1794 GCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCT 1853
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1929 GCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCT 1988

Qy      1854 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 1913
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1989 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 2048

Qy      1914 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 1973
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2049 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 2108

Qy      1974 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2033
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2109 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2168

Qy      2034 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2093
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2169 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2228

Qy      2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2153
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Db      2229 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2288

Qy      2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2289 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2348

Qy      2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2349 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2408

Qy      2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2409 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2468

Qy      2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2469 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2528

Qy      2394 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2529 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2588

Qy      2454 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2513
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2589 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2648

Qy      2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2573
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2649 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2708

Qy      2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2709 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2768

Qy      2634 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2693
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2769 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2828

Qy      2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
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Db      2829 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2868
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RESULT 9
US-10-094-886-115
; Sequence 115, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir

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;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Pochart, Pascal
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Spaderna, Steven
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-290 B
;  CURRENT APPLICATION NUMBER: US/10/094,886
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: 60/313,182
;  PRIOR FILING DATE: 2001-08-17
;  PRIOR APPLICATION NUMBER: 60/288,052
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/318,510
;  PRIOR FILING DATE: 2001-09-10
;  PRIOR APPLICATION NUMBER: 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: 60/314,018
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/274,194
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: 60/274,849
;  PRIOR FILING DATE: 2001-03-09
;  PRIOR APPLICATION NUMBER: 60/296,693
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: 60/313,626
;  PRIOR FILING DATE: 2001-08-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 298
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 115
;   LENGTH: 2898
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (21)..(2871)
US-10-094-886-115

  Query Match             82.6%;  Score 2260;  DB 17;  Length 2898;
  Best Local Similarity   90.7%;  Pred. No. 0;
  Matches 2562;  Conservative    0;  Mismatches   25;  Indels  237;  Gaps    5;

Qy       102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        98 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 157

Qy       162 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       158 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 217

Qy       222 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       218 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 277

Qy       282 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       278 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 337

Qy       342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       338 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 397

Qy       402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       398 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 457

Qy       462 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       458 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 517

Qy       522 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 581
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       518 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 577

Qy       582 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       578 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 637

Qy       642 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       638 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 697

Qy       702 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---------- 750
            ||||||||||||||||||||||||||||||||||||||||||||||||||          
Db       698 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGAATGGAGG 757

Qy       751 ---------------------------------------------------------- 750

Db       758 CTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAGAA 817

Qy       751 ---------------------------------------------------------- 750

Db       818 ACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTGAGGGAAT 877

Qy       751 -----------------------------------GTGGATGGGAGCTGGGAAGTGTG 773
                                                |||||||||||||||||||||||
Db       878 GTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 937

Qy       774 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 833
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       938 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 997

Qy       834 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 893
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Db       998 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 1057

Qy       894 CACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGC-- 951
            |||||||||||||||||||||| |   |  | || |||   ||         |       
Db      1058 CACAGATGGTCTTTGCATCCTAAACTCCACCACCATGCAGGAACCCAAGGTGACTGCCCT 1117

Qy       952 ----------------ATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 995
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Db      1118 TCAGACGCTATGCCAAATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 1177

Qy       996 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1055
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1178 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1237

Qy      1056 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1115
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Db      1238 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1297

Qy      1116 CTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTT 1175
            ||||||||||||||||||
Db      1298 CTTCAAAACAGTCCGTCAA---------------------------------------- 1316

Qy      1176 TGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1235
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1317 -GGGAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1375

Qy      1236 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1295
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Db      1376 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1435

Qy      1296 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1436 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1495
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Qy       1356 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1415
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1555

Qy       1416 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1475
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1615

Qy       1476 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1675

Qy       1536 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1595
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1735

Qy       1596 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGG 1655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG------GTCAGATGG 1789

Qy       1656 CTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCAC 1715
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Db       1790 CTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCAC 1849

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Db       1850 TCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCA 1909

Qy       1776 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1910 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1969

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Qy       1896 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 1955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2030 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 2089

Qy       1956 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2015
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Db       2090 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2149

Qy       2016 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2075
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Db       2150 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2209

Qy       2076 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2135
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Db       2210 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2269

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Db       2270 CCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCC 2329

Qy       2196 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2330 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2389

Qy       2256 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2315
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Db       2390 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2449

Qy       2316 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2375
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Db       2450 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2509

Qy       2376 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2510 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2569

Qy       2436 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2495
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Db       2570 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2629

Qy       2496 CTGGCAGATGTTAGCACAGAAAAACAGCATCAAC---AGGAATTTATCTTATTTCGCTAC 2552
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Db       2630 CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAGGAATTTATCTTATTTCGCTAC 2689

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Db       2750 TGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTC 2809

Qy       2673 AAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACT 2732
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RESULT 10
US-10-872-681-53
; Sequence 53, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209WO
; CURRENT APPLICATION NUMBER: US/10/872,681
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 53
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:31
US-10-872-681-53

Query Match 81.1%; Score 2220; DB 19; Length 2661;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

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Qy        184 GATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCCATG 243
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Qy        304 ACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAA 363
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Qy        364 CAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCAC 423
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Qy        424 CTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTT 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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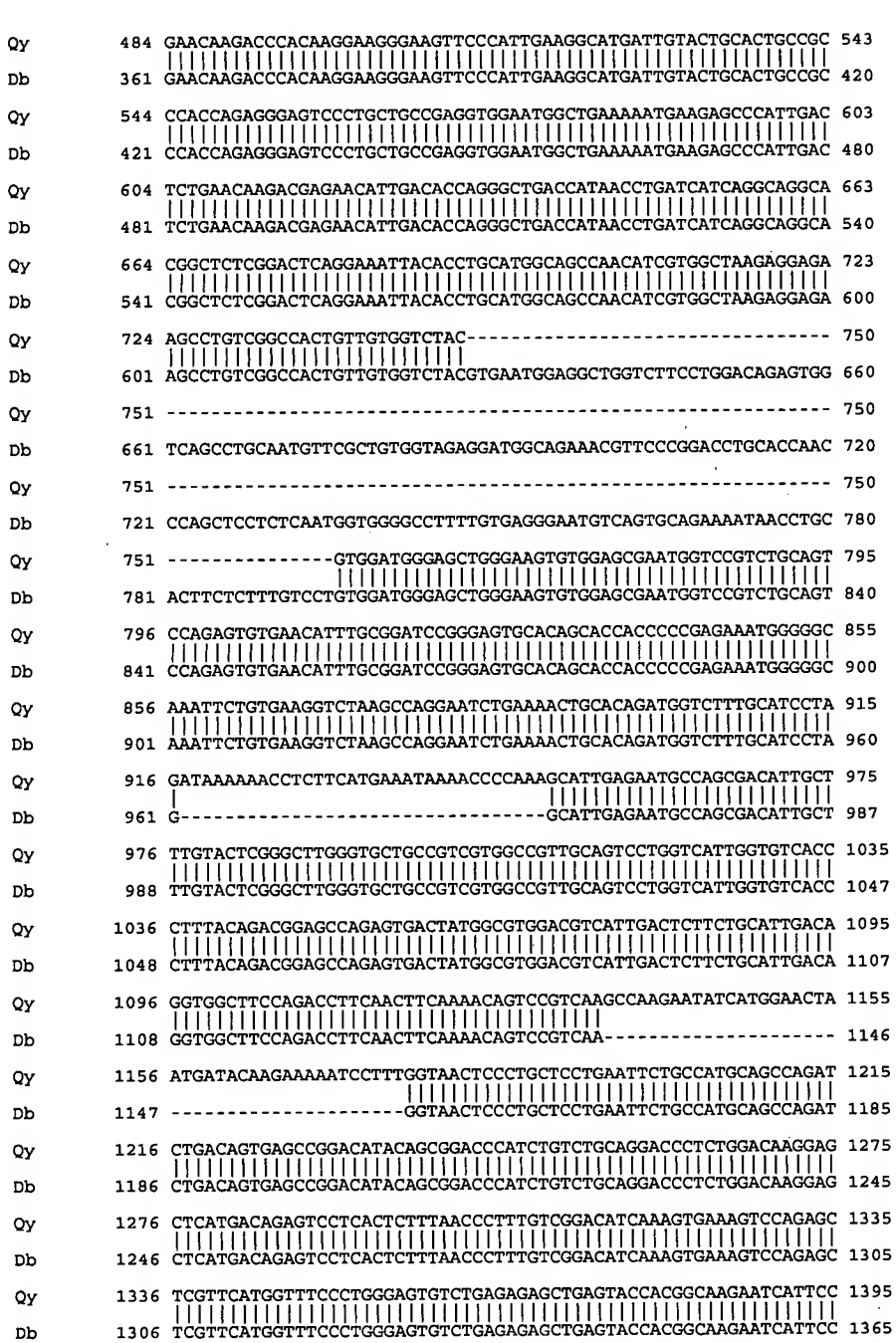
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Qy 544 CCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTGAC 603
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Qy 1216 CTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAG 1275
Db 1186 CTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAG 1245
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Db 1246 CTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGC 1305
Qy 1336 TCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCC 1395
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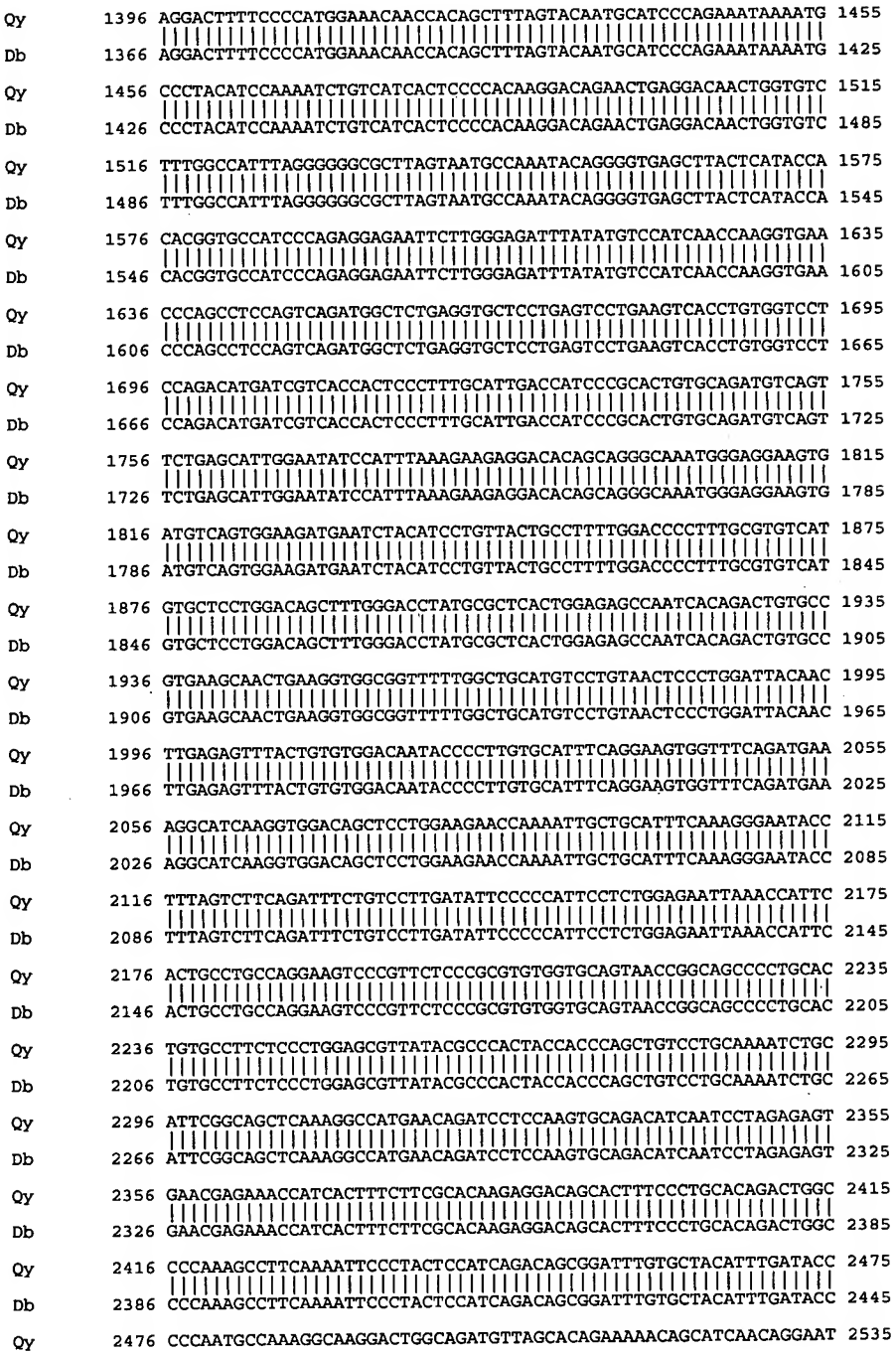
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Qy 1456 CCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTC 1515
Db 1426 CCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTC 1485
Qy 1516 TTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1575
Db 1486 TTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCA 1545
Qy 1576 CACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAA 1635
Db 1546 CACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAA 1605
Qy 1636 CCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCT 1695
Db 1606 CCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCT 1665
Qy 1696 CCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGT 1755
Db 1666 CCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGT 1725
Qy 1756 TCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTG 1815
Db 1726 TCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTG 1785
Qy 1816 ATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCAT 1875
Db 1786 ATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCAT 1845
Qy 1876 GTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCC 1935
Db 1846 GTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCC 1905
Qy 1936 GTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAAC 1995
Db 1906 GTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAAC 1965
Qy 1996 TTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAA 2055
Db 1966 TTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAA 2025
Qy 2056 AGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACC 2115
Db 2026 AGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACC 2085
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Db 2086 TTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTC 2145
Qy 2176 ACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCAC 2235
Db 2146 ACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCAC 2205
Qy 2236 TGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGC 2295
Db 2206 TGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGC 2265
Qy 2296 ATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGT 2355
Db 2266 ATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGT 2325
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Db 2326 GAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGC 2385
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Db 2386 CCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACC 2445
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RESULT 11
US-10-798-721-25
; Sequence 25, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/10/798,721
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: US/09/969,532
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 2043
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-798-721-25

  Query Match             74.7%;  Score 2043;  DB 18;  Length 2043;
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  Matches 2043;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 240

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 420

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 480

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 540

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 600

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 660

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 720

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 780

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 840

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
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Db        841 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 900

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 960

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1020

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1080

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1140

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1200

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1260

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1320

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1380

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1440

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1500

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1560
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Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1620

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1680

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1740

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1800

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1860

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1920

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1980

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2040

Qy       2734 TAG 2736
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Db       2041 TAG 2043
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RESULT 12
US-10-798-721-27
; Sequence 27, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/10/798,721
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: US/09/969,532
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 2010
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-798-721-27

  Query Match             71.9%;  Score 1967;  DB 18;  Length 2010;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;
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Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
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Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120
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Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG---------------- 223

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ----------------GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 267

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 327

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 387

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 447

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 507

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 567

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 627

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 687

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 747

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 807

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 867

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 927

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 987

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1047

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1107

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1167

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1227

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1287

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1347

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1407

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1467

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1527

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1587

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1647

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
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Db       1648 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1707

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
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Db       1708 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1767

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1827

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1828 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1887

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1947

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2007

Qy       2734 TAG 2736
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Db       2008 TAG 2010


RESULT 13
US-10-798-721-29
; Sequence 29, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Scoville, John
;  TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the Sa
;  FILE REFERENCE: LEX-0244-USA
;  CURRENT APPLICATION NUMBER: US/10/798,721
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: US/09/969,532
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US 60/237,280
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 2001
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-798-721-29

  Query Match             71.2%;  Score 1949;  DB 18;  Length 2001;
  Best Local Similarity   97.9%;  Pred. No. 0;
  Matches 2001;  Conservative    0;  Mismatches    0;  Indels   42;  Gaps    1;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
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Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 240

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 420

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
                 ||||||||||||||||||||
Db        421 AACTTCAAAACAGTCCGTCAA---------------------------------------- 441

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 ---GGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 498

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 558

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 618

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 678

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 738

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 798

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 858
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Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 918

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 978

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1038

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1098

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1158

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1218

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1278

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1338

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1398

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1458

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1459 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1518

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1519 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1578

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1638

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1639 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1698

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1758

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1818

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1878

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1938
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Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 1998

Qy       2734 TAG 2736
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Db       1999 TAG 2001
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RESULT 14
US-10-798-721-31
; Sequence 31, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-31

Query Match 68.5%; Score 1873; DB 18; Length 1968;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1968; Conservative 0; Mismatches 0; Indels 75; Gaps 2;

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Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 60

Qy        754 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTG 120

Qy        814 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTA 180

Qy        874 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCAT 933
              ||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAG---------------- 223

Qy        934 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 993
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 ----------------GCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 267

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 327

Qy       1054 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTC 387

Qy       1114 AACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCC 1173
              ||||||||||||||||||||
Db        388 AACTTCAAAACAGTCCGTCAA---------------------------------------- 408

Qy       1174 TTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 1233
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        409 ---GGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACA 465

Qy       1234 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 1293
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Db        466 TACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCA 525

Qy       1294 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 1353
Db        526 CTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTG 585

Qy       1354 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 1413
Db        586 GGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGA 645

Qy       1414 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 1473
Db        646 AACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTG 705

Qy       1474 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 1533
Db        706 TCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGG 765

Qy       1534 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 1593
Db        766 CGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAG 825

Qy       1594 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 1653
Db        826 GAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGAT 885

Qy       1654 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 1713
Db        886 GGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACC 945

Qy       1714 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1773
Db        946 ACTCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATC 1005

Qy       1774 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1833
Db        1006 CATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAA 1065

Qy       1834 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1893
Db        1066 TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTT 1125

Qy       1894 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1953
Db        1126 GGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTG 1185

Qy       1954 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 2013
Db        1186 GCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTG 1245

Qy       2014 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 2073
Db        1246 GACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAG 1305

Qy       2074 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 2133
Db        1306 CTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCT 1365

Qy       2134 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 2193
Db        1366 GTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTC 1425

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253
Db        1426 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 1485

Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313
Db        1486 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 1545

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373
Db        1546 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 1605

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433
Db        1606 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 1665

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493
Db        1666 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 1725

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553
Db        1726 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 1785

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613
Db        1786 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 1845

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673
Db        1846 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 1905

Qy       2674 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
Db        1906 AACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 1965

Qy       2734 TAG 2736
Db        1966 TAG 1968
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RESULT 15
US-10-798-721-1
; Sequence 1, Application US/10798721
; Publication No. US20040248166A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding the S
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/10/798,721
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-798-721-1

Query Match 59.9%; Score 1640; DB 18; Length 1734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
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Qy       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
Db       241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300

Qy       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
Db       301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
Db       361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
Db       421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480

Qy       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
Db       481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
Db       541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600

Qy       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660
Db       601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
Db       661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
Db       721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
Db       781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840

Qy       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
Db       841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy       901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
Db       901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960

Qy       961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db       961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020

Qy      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db      1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080

Qy      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db      1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140

Qy      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db      1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200

Qy      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db      1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260

Qy      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db      1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320

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Qy      1621 ATCAACCAAGGTGAACCCAG 1640
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Search completed: April 1, 2005, 06:11:22
Job time : 1527 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 20:54:14 ; Search time 11586 Seconds
(without alignments)
11442.557 Million cell updates/sec

Title: US-10-798-721-9
Perfect score: 2736
Sequence: 1 atggggagagcggcggccac.....gcaggcaaaatggactctag 2736

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2462.4	90.0	3252	9	AY358147	AY358147 Homo sapi
2	2365.2	86.4	7002	6	BD162193	BD162193 Novel unc
3	2365.2	86.4	7002	9	AB055056	AB055056 Homo sapi
4	2284	83.5	2868	6	AX800719	AX800719 Sequence
5	2220	81.1	2661	6	AX800717	AX800717 Sequence
6	1982.6	72.5	3925	10	MMU487854	AJ487854 Mus muscu
7	1599.8	58.5	2448	6	CQ841583	CQ841583 Sequence
8	1599.8	58.5	2448	9	AK122610	AK122610 Homo sapi
9	641.6	23.5	2625	6	CQ721377	CQ721377 Sequence
10	638.4	23.3	2585	6	CQ842137	CQ842137 Sequence
11	638.4	23.3	2585	9	AK122615	AK122615 Homo sapi
12	597	21.8	2860	6	AX686445	AX686445 Sequence
13	592.2	21.6	2860	6	AX686447	AX686447 Sequence
14	590.2	21.6	3933	6	CQ850929	CQ850929 Sequence
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16	590.2	21.6	3935	9	AB096256	AB096256 Homo sapi
17	589	21.5	3770	9	AY126437	AY126437 Homo sapi
18	588.6	21.5	3884	6	AR528525	AR528525 Sequence
19	588.6	21.5	3884	6	AX464012	AX464012 Sequence
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21	572.4	20.9	2895	6	AX512281	AX512281 Sequence
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25	563.2	20.6	2838	10	RNU87306	U87306 Rattus norv
26	554	20.2	2832	5	AY099459	AY099459 Xenopus l
27	544	19.9	2831	6	BD057526	BD057526 Netrin re
28	537	19.6	2995	6	AX497288	AX497288 Sequence
29	527.4	19.3	9328	10	AB118026	AB118026 Rattus no
30	520.6	19.0	2962	5	AY187310	AY187310 Gallus ga
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45	399.8	14.6	2406	6	AX833115	AX833115 Sequence

ALIGNMENTS

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DEFINITION Homo sapiens clone DNA219246 UNC5D (UNQ6012) mRNA, complete cds.
ACCESSION AY358147
VERSION AY358147.1 GI:37181401
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3252)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 3252)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES Location/Qualifiers
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gene 1. .3252
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ORIGIN

  Query Match            90.0%;  Score 2462.4;  DB 9;  Length 3252;
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  Matches 2693;  Conservative    0;  Mismatches    1;  Indels  210;  Gaps    2;

Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
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Qy       2593 GCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCCTTGAAGAGATTGGG 2652
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Db       3047 GCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCCTTGAAGAGATTGGG 3106

Qy       2653 AGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAAC 2712
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3107 AGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAAC 3166
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Qy       2713 TACAGCAGGCAAAATGGACTCTAG 2736
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Db       3167 TACAGCAGGCAAAATGGACTCTAG 3190
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RESULT 2
BD162193
LOCUS       BD162193               7002 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel unc5H4 gene and protein encoded thereby.
ACCESSION   BD162193
VERSION     BD162193.1  GI:27867951
KEYWORDS    JP 2002153290-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7002)
  AUTHORS   Ohara,O., Nagase,T., Nakayama,M. and Nakajima,D.
  TITLE     Novel unc5H4 gene and protein encoded thereby
  JOURNAL   Patent: JP 2002153290-A 1 28-MAY-2002;
            KAZUSA DNA RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002153290-A/1
            PD   28-MAY-2002
            PF   19-DEC-2000 JP 2000385090
            PI   OSAMU OHARA,TAKAHIRO NAGASE,MANABU NAKAYAMA,DAISUKE NAKAJIMA
            PC   C12N15/09,C07K14/705,C12N15/00
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                 Location/Qualifiers
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FEATURES              Location/Qualifiers
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ORIGIN
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Db        135 CTTCACCAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 194

Qy        155 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        275 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 334
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Db        315 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 374

Qy        335 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 394
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Db        375 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 434

Qy        395 ATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTG 454
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Qy        455 TGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCA 514
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Qy        515 TTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGG 574
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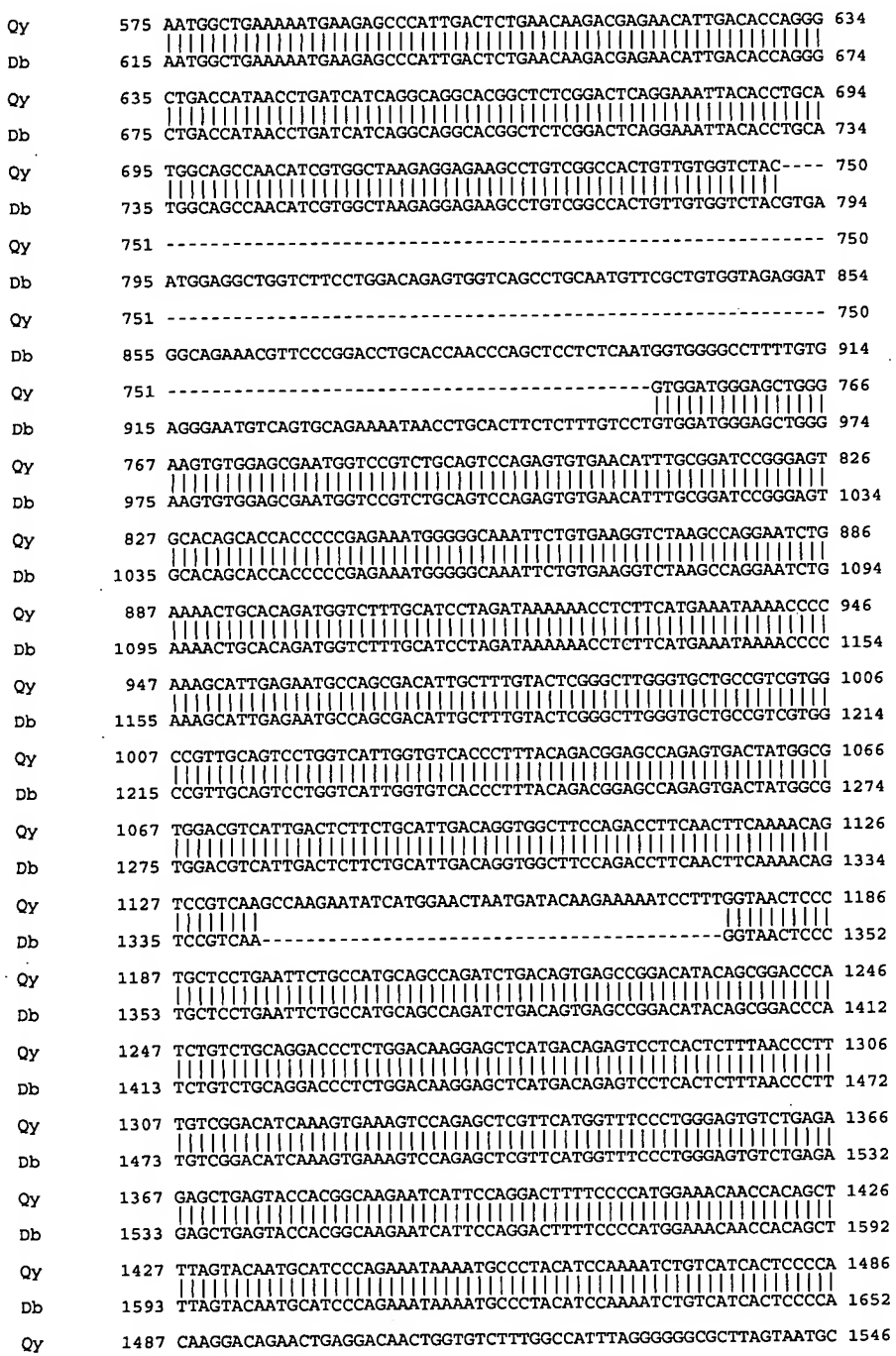
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Db 2013 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGC 2072
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Db 2073 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 2132
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Db 2433 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2492
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Qy 2387 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCA 2446
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Qy 2507 TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCAT 2566
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Qy       2687 CCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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RESULT 3
AB055056
LOCUS       AB055056               7002 bp    mRNA    linear   PRI 08-JAN-2002
DEFINITION  Homo sapiens mRNA for KIAA1777 protein (Unc5h4), complete cds.
ACCESSION   AB055056
VERSION     AB055056.1  GI:18150093
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakajima,D., Nakayama,M., Nagase,T. and Ohara,O.
  TITLE     Identification of unc5H4 gene
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 7002)
  AUTHORS   Nakajima,D., Nakayama,M., Nagase,T. and Ohara,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JAN-2001) Daisuke Nakajima, Kazusa DNA Research
            Institute, Laboratory for Genome Informatics; Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:nakajima@kazusa.or.jp, Tel:81438523915,
            Fax:81438523914)
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ORIGIN

  Query Match           86.4%;  Score 2365.2;  DB 9;  Length 7002;
  Best Local Similarity  92.4%;  Pred. No. 0;
  Matches 2597;  Conservative    0;  Mismatches    3;  Indels  210;  Gaps    2;

Qy         95 CTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 154
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Db        135 CTTCACCAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 194

Qy        155 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 214
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Qy        635 CTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCA 694
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Qy        751 -------------------------------------------GTGGATGGGAGCTGGG 766
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Qy       1007 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1066
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Qy       1367 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1426
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Qy       2267 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2326
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RESULT 4
AX800719
LOCUS AX800719 2868 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 55 from Patent WO03055915.
ACCESSION AX800719
VERSION AX800719.1 GI:37653770
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fitzgerald,S.N., Fagan,R.J., Phelps,C.B., Power,C. and Yorke,M.
TITLE Transmembrane protein
JOURNAL Patent: WO 03055915-A 55 10-JUL-2003;
ARES TRADING S.A. (CH)
FEATURES Location/Qualifiers
source 1. .2868
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ORIGIN

Query Match 83.5%; Score 2284; DB 6; Length 2868;
Best Local Similarity 91.3%; Pred. No. 0;
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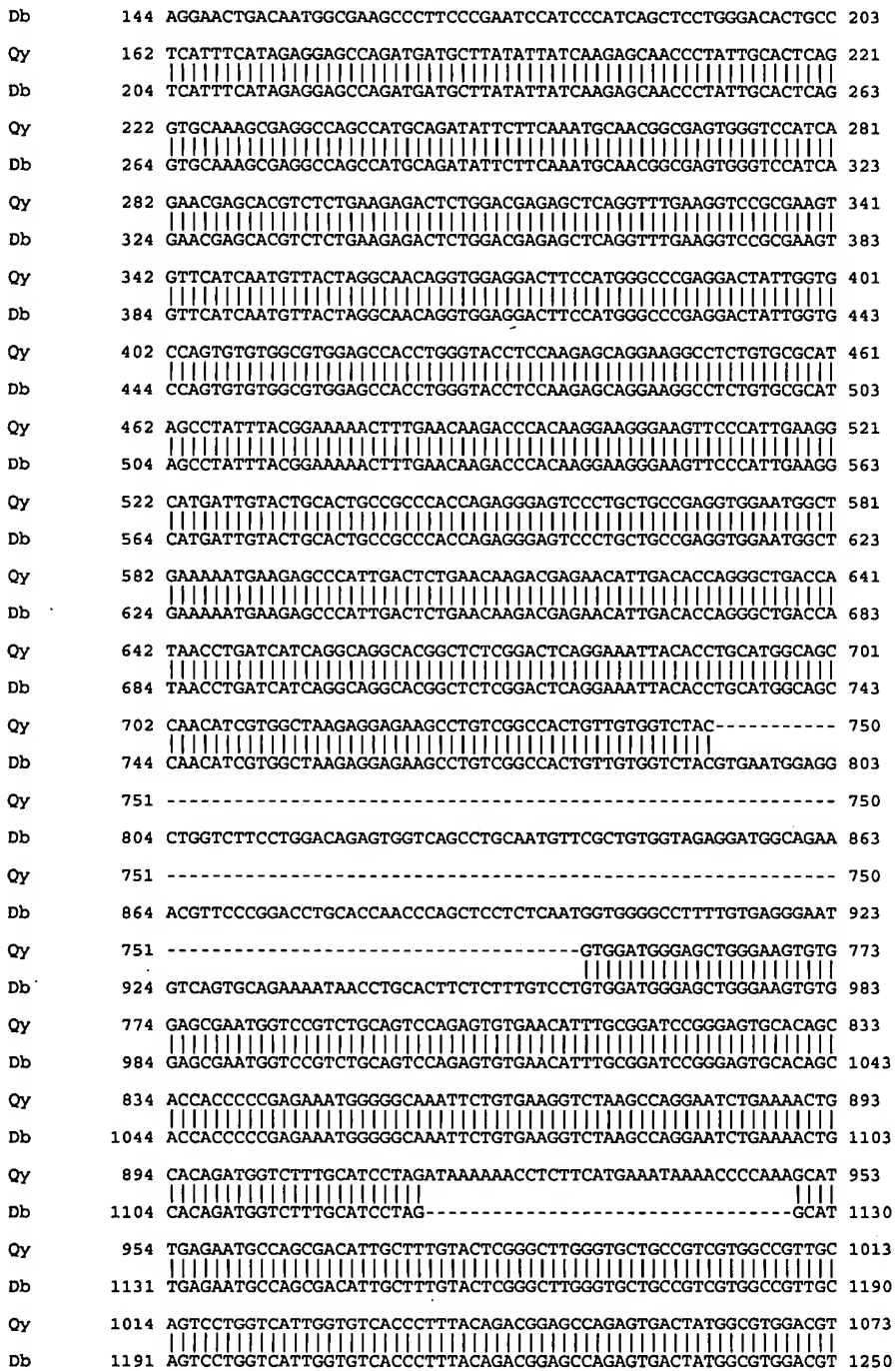
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RESULT 5
AX800717
LOCUS       AX800717               2661 bp    DNA     linear   PAT 13-OCT-2003
DEFINITION  Sequence 53 from Patent WO03055915.
ACCESSION   AX800717
VERSION     AX800717.1  GI:37653769
KEYWORDS    .
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REFERENCE   1
  AUTHORS   Fitzgerald,S.N., Fagan,R.J., Phelps,C.B., Power,C. and Yorke,M.
  TITLE     Transmembrane protein
  JOURNAL   Patent: WO 03055915-A 53 10-JUL-2003;
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ORIGIN

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Qy        544 CCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTGAC 603
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Qy        751 ---------------------------------------------------------- 750

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Qy        856 AAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTA 915
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Qy        916 GATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCT 975
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Db        961 G--------------------------------GCATTGAGAATGCCAGCGACATTGCT 987

Qy        976 TTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACC 1035
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Qy       1036 CTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACA 1095
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Qy       1216 CTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAG 1275
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RESULT 6
MMU487854
LOCUS       MMU487854              3925 bp    mRNA    linear   ROD 24-SEP-2002
DEFINITION  Mus musculus mRNA for netrin receptor Unc5h4 (Unc5h4 gene).
ACCESSION   AJ487854
VERSION     AJ487854.1  GI:22080675
KEYWORDS    netrin receptor Unc5h4; Unc5h4 gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Engelkamp,D.
  TITLE     Cloning of three mouse unc-5 genes and their expression patterns at
            mid-gestation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3925)
  AUTHORS   Engelkamp,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
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ORIGIN

Query Match 72.5%; Score 1982.6; DB 10; Length 3925;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 284; Indels 225; Gaps 3;

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Qy        3 GGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGGCT 62
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Qy     1260 CCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAA 1319
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Qy     1440 TCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACT 1499
Db     1874 TCCCAGAAACAAAACGCCGTACATCCAAAATCTGTCATCACTGCCGACAAGGACAGAGCT 1933

Qy     1500 GAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGT 1559
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Qy     1560 GAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTC 1619
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Qy     1620 CATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGA 1679
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Qy     1680 AGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCA 1739
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Qy       1860 CCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCC 1919
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Qy       1920 AATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAA 1979
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Db       3014 GAACCTCTGGGAAGCTCGTCATCAGCAGGATGGGGACCTCGACTCGCTCGCCTGTGCCCT 3073

Qy       2640 TGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGA 2699
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Db       3074 TGAGGAGATTGGGAGGACACACACGAAACTATCCAACATCACAGAGCCACAGATTGATGA 3133

Qy       2700 AGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
              || |||||||||||||||||||||||||||||||||
Db       3134 TGCTGACTTCAACTACAGCAGGCAAAATGGACTCTAG 3170


RESULT 7
CQ841583
LOCUS       CQ841583               2448 bp    DNA     linear   PAT 02-AUG-2004
DEFINITION  Sequence 230 from Patent EP1440981.
ACCESSION   CQ841583
VERSION     CQ841583.1  GI:50893370
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
  TITLE     Full-length human cdna
  JOURNAL   Patent: EP 1440981-A 230 28-JUL-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .2448
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             58.5%;  Score 1599.8;  DB 6;  Length 2448;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1134 AGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCT 1193
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Qy       1194 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1253
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Db        159 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 218

Qy       1254 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGA 1313
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        219 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTCAACCCTTTGTCGGA 278

Qy       1314 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 338

Qy       1374 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 1433
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Db        339 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 398

Qy       1434 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 1493
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Db        399 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 458

Qy       1494 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATAC 1553
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Db        459 AGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATAA 518

Qy       1554 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 1613
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Db        519 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 578

Qy       1614 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 1673
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Db        579 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 638

Qy       1674 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACCAT 1733
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Qy       1734 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1793
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Db        699 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 758

Qy       1794 GCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCT 1853
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Qy       1854 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 1913
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Db        819 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 878

Qy       1914 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 938

Qy       1974 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2033
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Db        939 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 998

Qy       2034 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2093
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Db        999 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 1058

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Db       1059 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 1118

Qy       2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213
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Db       1119 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 1178

Qy       2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273
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Db       1179 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 1238

Qy       2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333
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Db       1239 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 1298

Qy       2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393
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Db       1299 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 1358

Qy       2394 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2453
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Db       1359 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 1418

Qy       2454 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2513
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Db       1419 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 1478

Qy       2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2573
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Db       1479 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 1538

Qy       2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633
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Db       1539 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 1598

Qy       2634 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 1658

Qy       2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db       1659 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 1701
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RESULT 8
AK122610

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LOCUS       AK122610               2448 bp    mRNA    linear   PRI 09-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ16019 fis, clone BRAMY2001473, weakly similar
            to Rattus norvegicus transmembrane receptor Unc5H2 mRNA.
ACCESSION   AK122610
VERSION     AK122610.1  GI:34527786
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
            Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2448)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 58.5%; Score 1599.8; DB 9; Length 2448;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1601; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db         99 AGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCT 158

Qy       1194 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 1253
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Db        159 GAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCT 218

Qy       1254 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGA 1313
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Db        219 GCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTCAACCCTTTGTCGGA 278

Qy       1314 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 1373
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Db        279 CATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGA 338

Qy       1374 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 1433
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Db        339 GTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTAC 398

Qy       1434 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 1493
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Db        399 AATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGAC 458

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Qy       1554 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 1613
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Db        519 AGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTA 578
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Qy       1614 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 1673
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Db        579 TATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAG 638

Qy       1674 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 1733
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Db        639 TCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCAT 698

Qy       1734 CCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACA 1793
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Qy       2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213
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Qy       2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273
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Qy       2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393
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Db       1419 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 1478

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RESULT 9
CQ721377
LOCUS       CQ721377                2625 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 7311 from Patent WO02068579.
ACCESSION   CQ721377
VERSION     CQ721377.1  GI:42282234
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 7311 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             23.5%;  Score 641.6;  DB 6;  Length 2625;
  Best Local Similarity   56.9%;  Pred. No. 6.2e-166;
  Matches 1507;  Conservative    0;  Mismatches 1014;  Indels  127;  Gaps   13;

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Qy        122 CCCTTCCCGAATCCATCCCATCAGCTC---CTGGGACACTGCCTCATTTCATAGAGGAGC 178
Db         86 TGCTCCCTGACTCCTTCCCGTCAGCGCCAGCAGAGCCGCTGCCCTACTTCCTGCAGGAGC 145

Qy        179 CAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAG 238
Db        146 CACAGGACGCCTACATTGTGAAGAACAAGCCTGTGGAGCTCCGCTGCCGCGCCTTCCCCG 205

Qy        239 CCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTG 298
Db        206 CCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTCAGCCAGAACGACCACGTCACAC 265

Qy        299 AAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTA 358
Db        266 AGGAAGGCCTGGATGAGGCCACCGGCCTGCGGGTGCGCGAGGTGCAGATCGAGGTGTCGC 325

Qy        359 GGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGA 418
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Qy        419 GCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAA 478
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Qy        479 ACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACT 538
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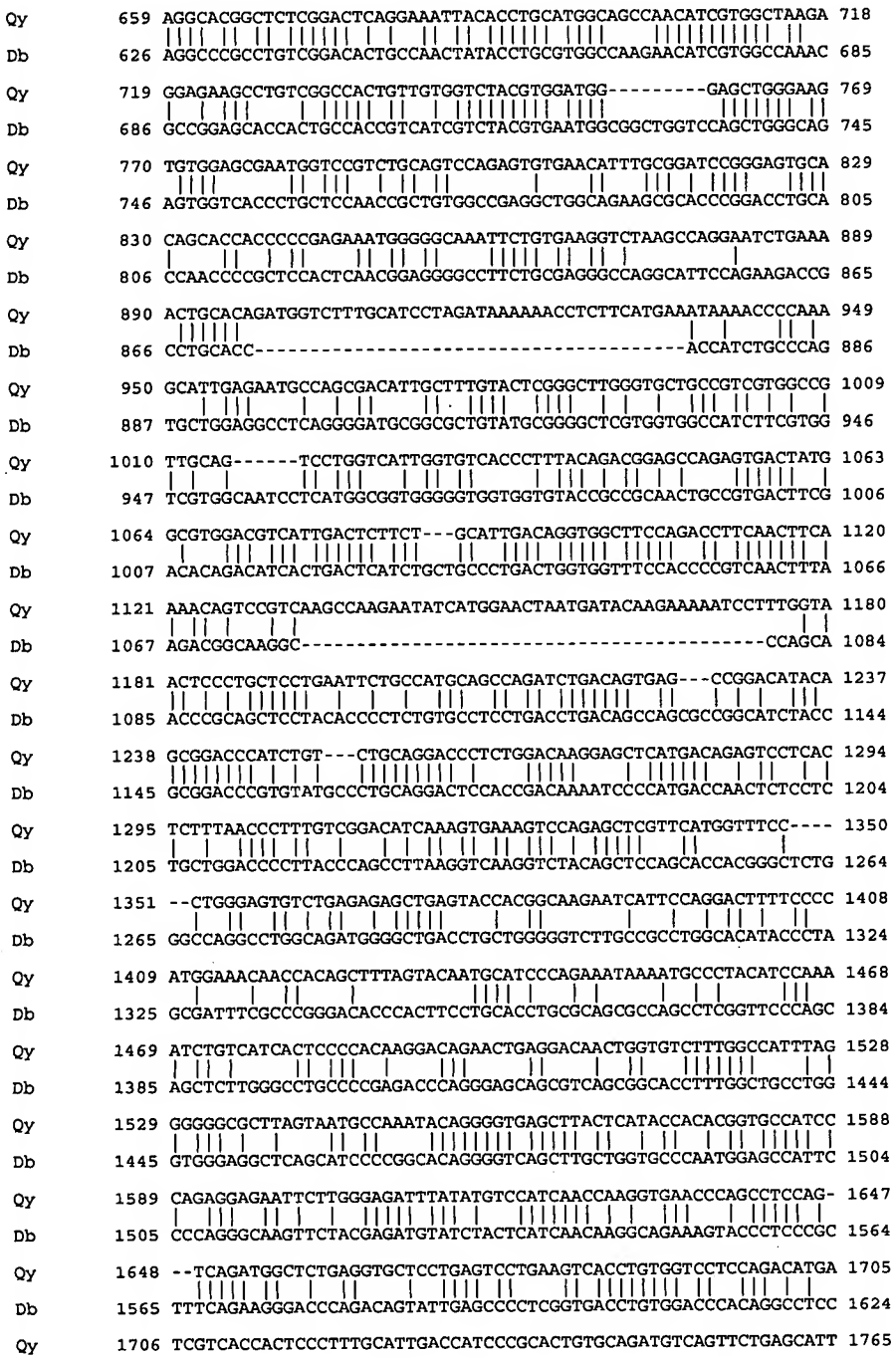

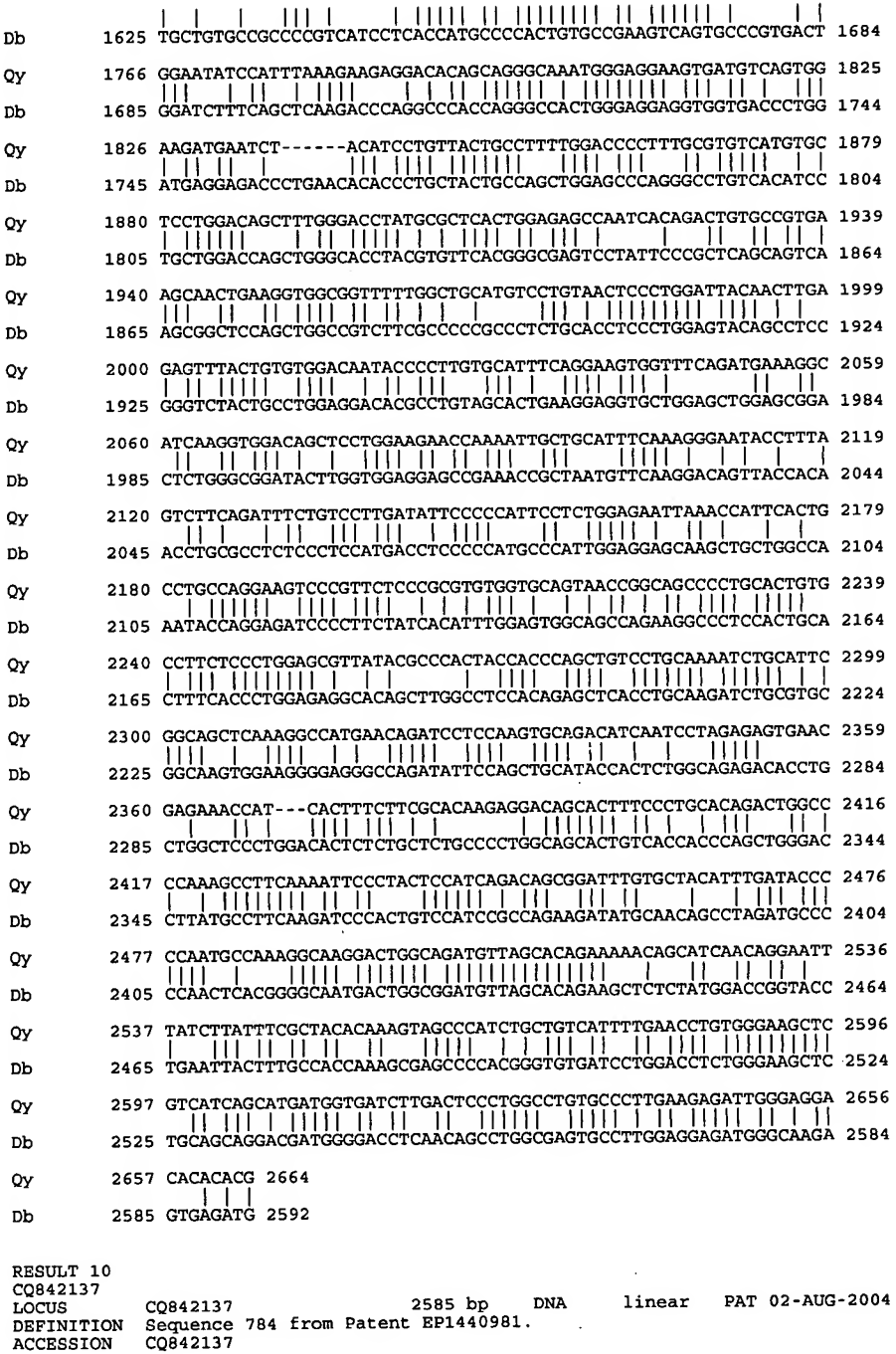

RESULT 10
CQ842137
LOCUS CQ842137 2585 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 784 from Patent EP1440981.
ACCESSION CQ842137

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VERSION     CQ842137.1  GI:50893924
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
  TITLE     Full-length human cdna
  JOURNAL   Patent: EP 1440981-A 784 28-JUL-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .2585
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ORIGIN

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  Matches  743;  Conservative    0;  Mismatches   16;  Indels   75;  Gaps    2;

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Db        298 CACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAG 357

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Qy       1455 GCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGT 1514
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Db        943 GCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGT 1002

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LOCUS       AK122615               2585 bp    mRNA    linear   PRI 09-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ16027 fis, clone FCBBF3012170, moderately
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            (rcm) mRNA.
ACCESSION   AK122615
VERSION     AK122615.1  GI:34527792
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K.,
            Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2585)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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ORIGIN

  Query Match             23.3%;  Score 638.4;  DB 9;  Length 2585;
  Best Local Similarity   89.1%;  Pred. No. 4.8e-165;
  Matches  743;  Conservative    0;  Mismatches   16;  Indels   75;  Gaps    2;

Qy        735 CACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAG 794
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Db        298 CACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAG 357

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Qy        855 CAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCT 914
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Qy       1335 CTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTC 1394
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Db        823 CTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTC 882

Qy       1395 CAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAAT 1454
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ACCESSION   AX686445
VERSION     AX686445.1  GI:29372153
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Edinger,S., Macdougall,J.R., Millet,I., Ellerman,K., Stone,D.J.,
            Gerlach,V., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Rieger,D.,
            Burgess,C.E., Casman,S.J., Spytek,K.A., Boldog,F.L., Li,L.,
            Padigaru,M., Mishra,V., Patturajan,M., Shenoy,S., Rastelli,L.,
            Tchernev,V.T., Vernet,C.A., Zerhusen,B.D., Malyankar,U.M., Guo,Y.,
            Miller,C.E. and Gangolli,E.A.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02057450-A 1 25-JUL-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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Qy      1993 AACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGAT 2052
Db      2153 AGCCTCCGGGTCTACTGCCTGGAGGACACGCCTGTAGCACTGAAGGAGGTGCTGGAGCTG 2212
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Qy      2113 ACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCA 2172
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Qy      2650 GGGAGGACACACACG 2664
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LOCUS       AX686447               2860 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 3 from Patent WO02057450.
ACCESSION   AX686447
VERSION     AX686447.1  GI:29372154
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Edinger,S., Macdougall,J.R., Millet,I., Ellerman,K., Stone,D.J.,
            Gerlach,V., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Rieger,D.,
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  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02057450-A 3 25-JUL-2002;
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Qy        373 GACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACC 432
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Qy        433 TCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGAC 492
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Qy        899 ------------------------ATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATG 934
Db       1013 GCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCCACCCCAGAACGGAGGCCGTGACTGC 1072

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Qy        995 CTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGA 1054
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Qy       1055 GTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGA-CCTTC 1113
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Qy       1231 ACATACAGCGGACCCATCTGT---CTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAG 1287
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Qy       1288 TCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCA----- 1342
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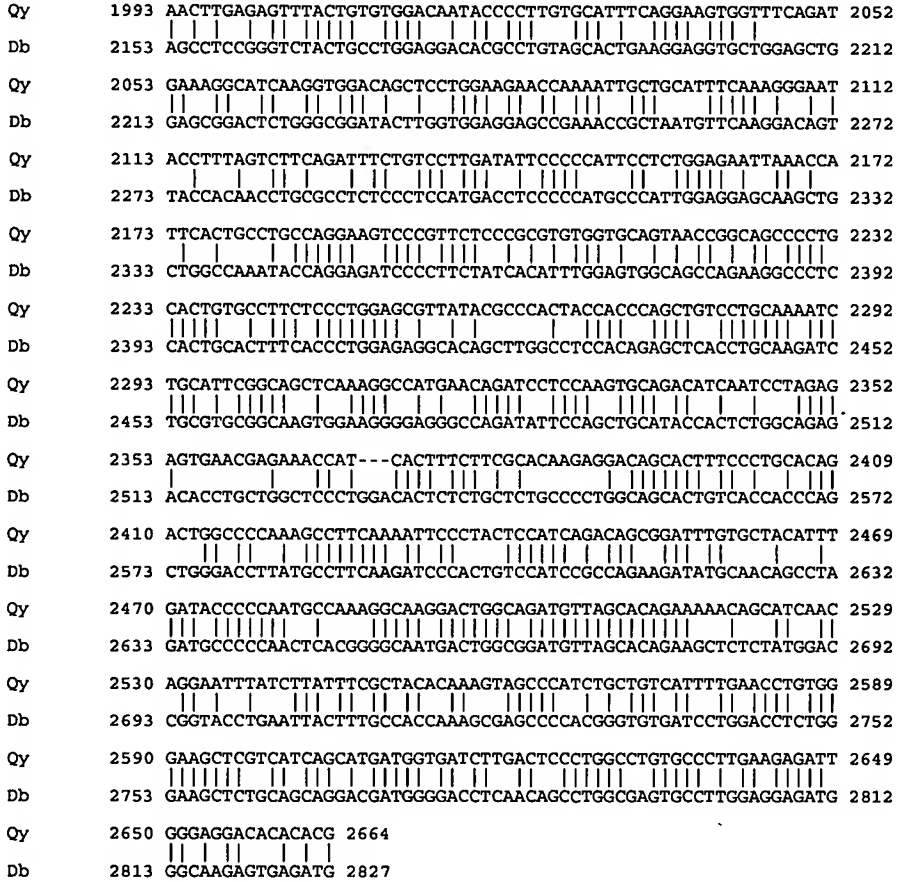

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Qy       2113 ACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCA 2172
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RESULT 14
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DEFINITION  Sequence 1398 from Patent EP1447413.
ACCESSION   CQ850929
VERSION     CQ850929.1  GI:51509141
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
            Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
  TITLE     Full-length human cDNA
  JOURNAL   Patent: EP 1447413-A 1398 18-AUG-2004;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
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Query Match 21.6%; Score 590.2; DB 6; Length 3933;
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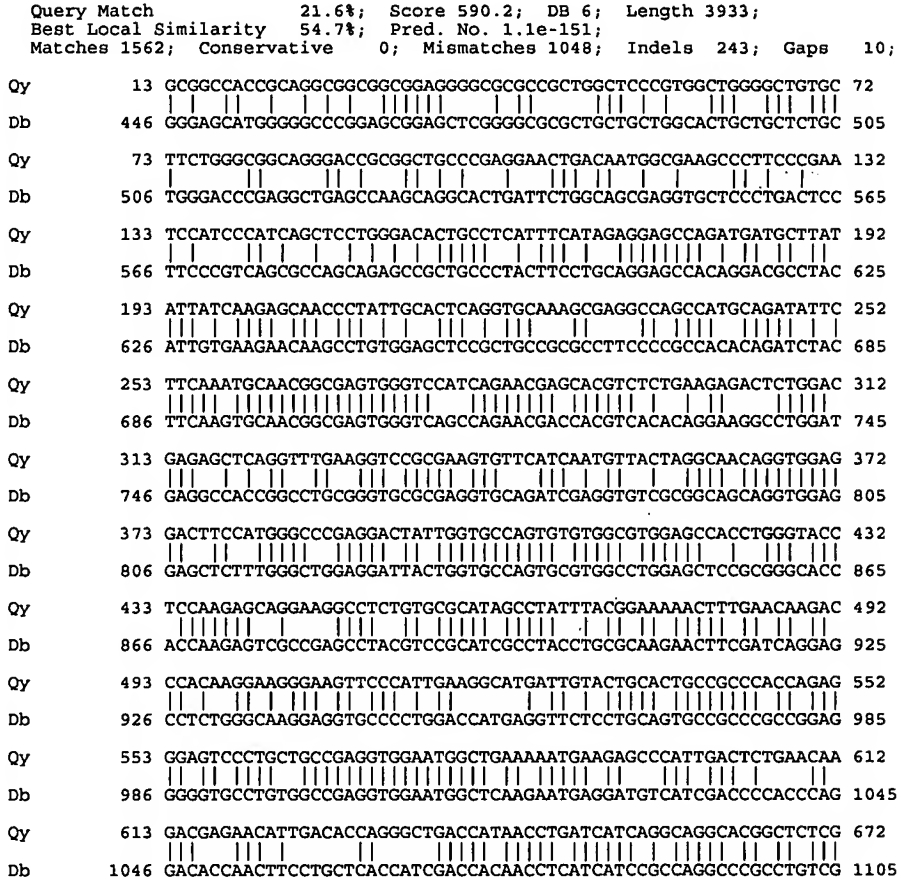

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Qy        805 GAACATTTGCGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGT 864
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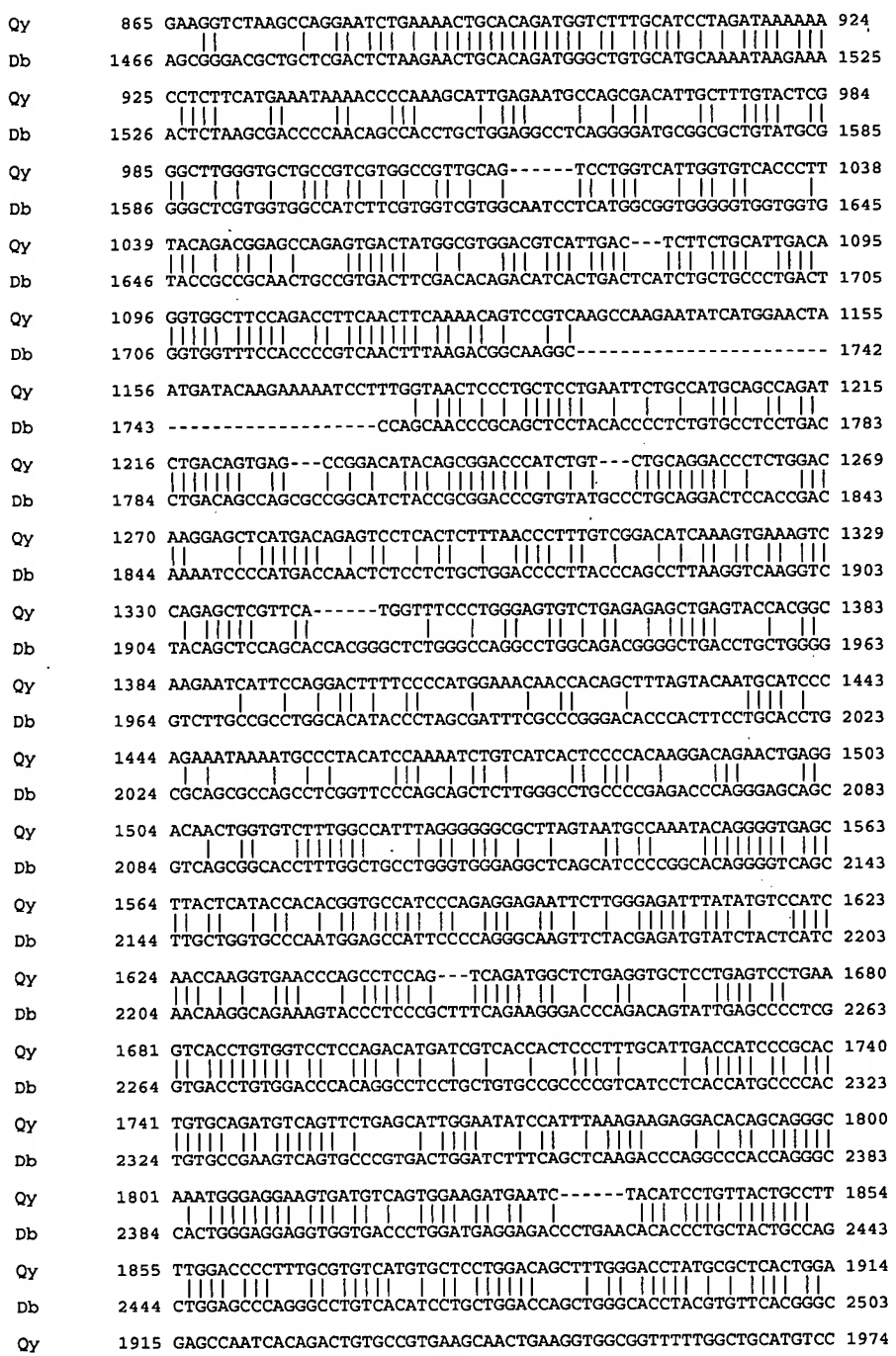

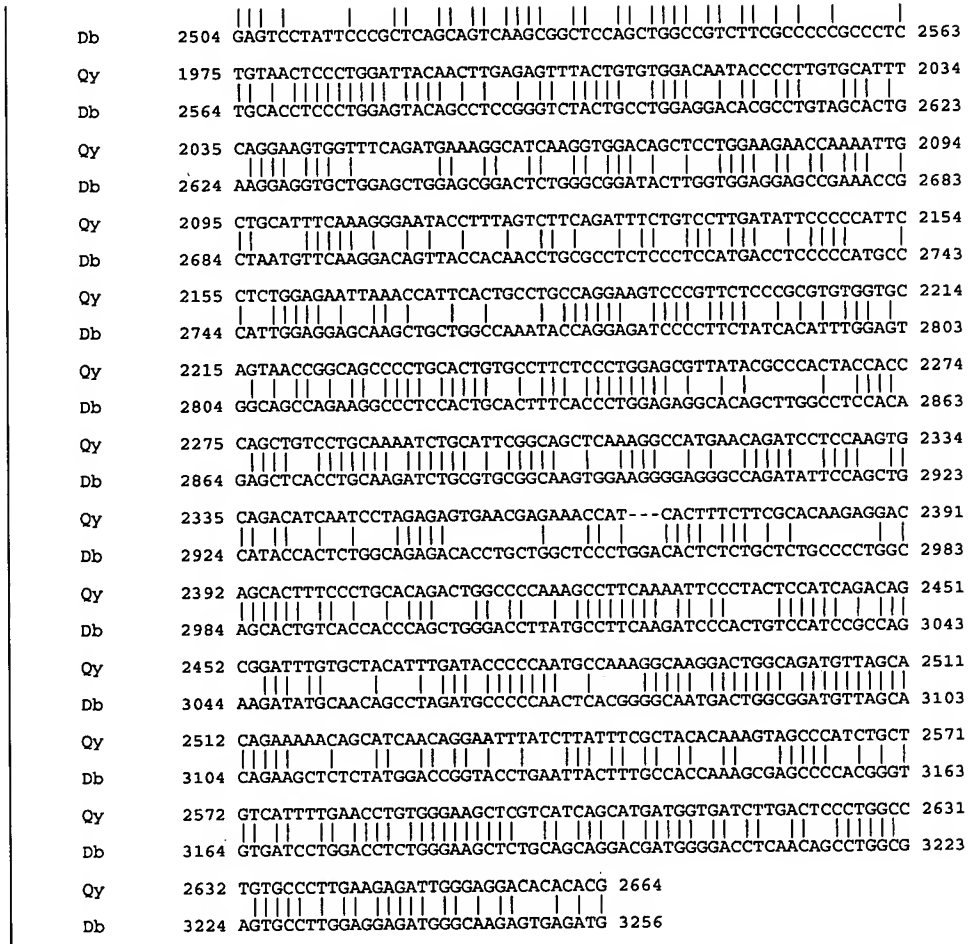

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ACCESSION AK128132
VERSION AK128132.1 GI:34535352
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE NEDO human cDNA sequencing project

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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3933)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
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            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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ORIGIN

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Qy         73 TTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAA 132
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Qy        133 TCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTAT 192
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Qy        253 TTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGAC 312
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Qy        373 GACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACC 432
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Qy        433 TCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGAC 492
Db        866 ACCAAGAGTCGCCGAGCCTACGTCCGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAG 925

Qy        493 CCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAG 552
Db        926 CCTCTGGGCAAGGAGGTGCCCCTGGACCATGAGGTTCTCCTGCAGTGCCGCCCGCCGGAG 985

Qy        553 GGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAA 612
Db        986 GGGGTGCCTGTGGCCGAGGTGGAATGGCTCAAGAATGAGGATGTCATCGACCCCACCCAG 1045

Qy        613 GACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCG 672
Db       1046 GACACCAACTTCCTGCTCACCATCGACCACAACCTCATCATCCGCCAGGCCCGCCTGTCG 1105

Qy        673 GACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCG 732
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Qy        768 ------------------------------------------------------------ 767
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Qy        805 GAACATTTGCGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGT 864
Db       1406 GCCCACTGGCGTAGCCGCGAGTGCATGGCGCCCCCACCCCAGAACGGAGGCCGTGACTGC 1465

Qy        865 GAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAA 924
Db       1466 AGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAA 1525

Qy        925 CCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCG 984
Db       1526 ACTCTAAGCGACCCCAACAGCCACCTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCG 1585

Qy        985 GGCTTGGGTGCTGCCGTCGTGGCCGTTGCAG------TCCTGGTCATTGGTGTCACCCTT 1038
Db       1586 GGGCTCGTGGTGGCCATCTTCGTGGTCGTGGCAATCCTCATGGCGGTGGGGGTGGTGGTG 1645

Qy       1039 TACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC---TCTTCTGCATTGACA 1095
Db       1646 TACCGCCGCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGACT 1705

Qy       1096 GGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTA 1155
Db       1706 GGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGC----------------------- 1742

Qy       1156 ATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGAT 1215
Db       1743 ------------------CCAGCAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGAC 1783

Qy       1216 CTGACAGTGAG---CCGGACATACAGCGGACCCATCTGT---CTGCAGGACCCTCTGGAC 1269
Db       1784 CTGACAGCCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGAC 1843

Qy       1270 AAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTC 1329
Db       1844 AAAATCCCCATGACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTC 1903

Qy       1330 CAGAGCTCGTTCA------TGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGC 1383
Db       1904 TACAGCTCCAGCACCACGGGCTCTGGGCCAGGCCTGGCAGACGGGGCTGACCTGCTGGGG 1963

Qy       1384 AAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCC 1443
Db       1964 GTCTTGCCGCCTGGCACATACCCTAGCGATTTCGCCCGGGACACCCACTTCCTGCACCTG 2023

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Qy       1504 ACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGC 1563
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Qy      1564 TTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATC 1623
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Db      2144 TTGCTGGTGCCCAATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTATCTACTCATC 2203

Qy      1624 AACCAAGGTGAACCCAGCCTCCAG---TCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
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Db      2204 AACAAGGCAGAAAGTACCCTCCCGCTTTCAGAAGGGACCCAGACAGTATTGAGCCCCTCG 2263

Qy      1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCAC 1740
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Db      2264 GTGACCTGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCGTCATCCTCACCATGCCCCAC 2323

Qy      1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
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Db      2324 TGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCCACCAGGGC 2383

Qy      1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC------TACATCCTGTTACTGCCTT 1854
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Db      2384 CACTGGGAGGAGGTGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAG 2443

Qy      1855 TTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGA 1914
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Qy      2035 CAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTG 2094
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Db      2624 AAGGAGGTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCG 2683

Qy      2095 CTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTC 2154
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Db      2684 CTAATGTTCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCC 2743

Qy      2155 CTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGC 2214
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Qy      2275 CAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTG 2334
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Qy      2335 CAGACATCAATCCTAGAGAGTGAACGAGAAACCAT---CACTTTCTTCGCACAAGAGGAC 2391
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Qy      2512 CAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCT 2571
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Search completed: April 1, 2005, 05:14:27
Job time : 11613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 18:01:54 ; Search time 8583 Seconds
(without alignments)
12133.734 Million cell updates/sec

Title: US-10-798-721-9
Perfect score: 2736
Sequence: 1 atggggagagcggcggccac.....gcaggcaaaatggactctag 2736

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2202	80.5	2775	9	AY401469	AY401469 Homo sapi
	2	1871.4	68.4	2507	9	AY401470	AY401470 Pan trogl
	3	1796	65.6	2775	9	AY401471	AY401471 Mus muscu
	4	565.8	20.7	3866	3	AK018177	AK018177 Mus muscu
	5	529.4	19.3	532	6	CD636011	CD636011 56033904H
c	6	529.4	19.3	596	6	CD636014	CD636014 56033928J
c	7	517.4	18.9	530	6	CD636012	CD636012 56033904J
	8	501.2	18.3	2802	9	AY406491	AY406491 Homo sapi
	9	491.6	18.0	2532	9	AY411747	AY411747 Homo sapi
	10	476.4	17.4	3790	3	AK031655	AK031655 Mus muscu
	11	475.2	17.4	2791	9	AY406493	AY406493 Mus muscu
	12	471.8	17.2	2532	9	AY411749	AY411749 Mus muscu
c	13	440	16.1	812	5	BX915627	BX915627 BX915627
	14	434.2	15.9	2532	9	AY411748	AY411748 Pan trogl
	15	386.2	14.1	896	5	BU447189	BU447189 603214135
	16	372	13.6	445	5	BY291669	BY291669 BY291669
	17	368	13.5	392	6	CD636013	CD636013 56033928H
	18	360.6	13.2	2802	9	AY406492	AY406492 Pan trogl
	19	318	11.6	413	4	BM726542	BM726542 UI-E-EJ0-
c	20	312.6	11.4	567	2	BF390834	BF390834 UI-R-CA1-
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c	23	283.2	10.4	390	5	BU729454	BU729454 UI-E-CL1-
	24	282	10.3	378	4	BM702977	BM702977 UI-E-CL1-
	25	281	10.3	818	4	BI818609	BI818609 603033362
	26	275.2	10.1	1034	4	BI758231	BI758231 603029876
	27	274.2	10.0	1175	2	BF530640	BF530640 602071931
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	29	265.2	9.7	749	7	CF735417	CF735417 UI-M-HB0-
	30	262.2	9.6	751	7	CF735550	CF735550 UI-M-HB0-
c	31	261	9.5	733	5	BX920046	BX920046 BX920046
	32	260.8	9.5	577	9	CC469639	CC469639 CH240_142
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ALIGNMENTS

RESULT 1
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LOCUS AY401469 2775 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401469
VERSION AY401469.1 GI:39757458
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2775)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2775)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
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gene <1. .>2775
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ORIGIN

Query Match 80.5%; Score 2202; DB 9; Length 2775;
Best Local Similarity 88.3%; Pred. No. 0;
Matches 2475; Conservative 0; Mismatches 85; Indels 243; Gaps 3;

Qy 102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161
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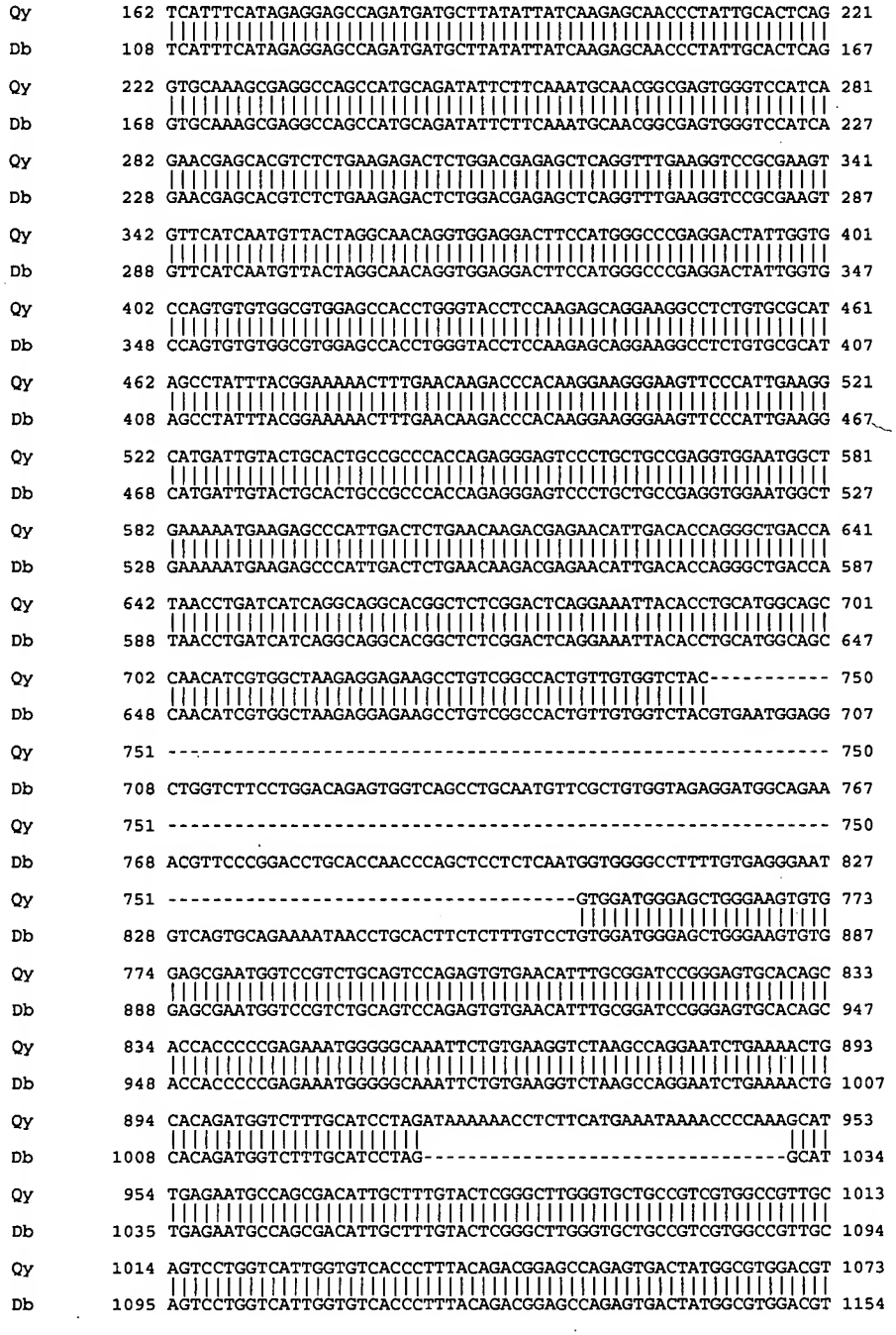
Db 48 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 107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Db 1893 TTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGG 1952
Qy 1914 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 1973
Db 1953 AGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTC 2012
Qy 1974 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2033
Db 2013 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2072
Qy 2034 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2093
Db 2073 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2132
Qy 2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2153
Db 2133 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2192
Qy 2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213

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Db       2193 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2252

Qy       2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2253 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2312

Qy       2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2313 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2372

Qy       2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2373 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2432

Qy       2394 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2433 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2492

Qy       2454 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2513
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2493 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2552

Qy       2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2553 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2612

Qy       2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633
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Db       2613 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2672

Qy       2634 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2693
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2673 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2732

Qy       2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
             |||||||||||||||||||||||||||||||||||||||||||
Db       2733 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2775


RESULT 2
AY401470
LOCUS       AY401470               2507 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401470
VERSION     AY401470.1  GI:39757459
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2507)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2507)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2507
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>2507
                     /locus_tag="HCM0901"
ORIGIN

  Query Match             68.4%;  Score 1871.4;  DB 9;  Length 2507;
  Best Local Similarity   83.3%;  Pred. No. 0;
  Matches 2124;  Conservative    0;  Mismatches  248;  Indels  177;  Gaps    3;

Qy        323 GTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATG 382
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          1 GTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACCAGGCAACAGGTGGAGGACTTCCATG 60

Qy        383 GGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCA 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCA 120

Qy        443 GGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAA 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAA 180

Qy        503 GGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTG 562
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGAGGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTG 240

Qy        563 CTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACA 622
              ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCNNNNGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACA 300

Qy        623 TTGACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAA 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTGACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAA 360

Qy        683 ATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTG 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTG 420

Qy        743 TGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGT 802
              |||||||||| |||| |||||      |||| || ||||| | ||||| |      |
Db        421 TGGTCTACGTGAATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCT 480

Qy        803 GTG---------AACATTTGCGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGG 853
              |||         ||    ||   ||||  |||||    ||| | ||    ||||| |
Db        481 GTGGTAGAGGATGGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTG 540

Qy        854 GCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCAC---------------- 896
              |    || |||| ||  |      | |      || ||||||
Db        541 GGGCCTTTTGTGAGGGAATGTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGNNN 600

Qy        897 ------------------------------------------------------------ 896

Db        601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660

Qy        897 ----------------------------------------------AGATGGTCTTT 907

Db        661 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy        908 GCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCG 967
                                                  ||||||||||||||||||
Db        721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCATTGAGAATGCCAGCG 780

Qy        968 ACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTG 1027
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        781 ACATTGCTTTGTACTCGGGCTTGGGCGCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTG 840

Qy       1028 GTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTG 1087
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Db        841 GTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTG 900

Qy       1088 CATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAGAATATCA 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 CATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAA---------- 947

Qy       1148 TGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGC 1207
                                  |   |||||||||||||||||| |||||||
Db        948 ----------------------------GNNNACTCCCTGCTCCTGAATTCCGCCATGC 978

Qy       1208 AGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGG 1267
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 AGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGG 1038

Qy       1268 ACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAG 1327
              |||||||||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db       1039 ACAAGGAGCTCATGACAGAGTCCTCACTGTTTAACCCTTTGTCGGACATCAAAGTCAAAG 1098

Qy       1328 TCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGA 1387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 TCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGA 1158

Qy       1388 ATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAA 1447
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 ATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAA 1218

Qy       1448 ATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAA 1507
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 ATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAA 1278

Qy       1508 CTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTAC 1567
              |||||||||   |||||||||||||||
Db       1279 CTGGTGTCTNNNGCCATTTAGGGGGGCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1338

Qy       1568 TCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACC 1627

Db       1339 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1398

Qy       1628 AAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCT 1687
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 NNNNNNNNNNNNNCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCT 1458

Qy       1688 GTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCACTGTGCAG 1747
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1459 GTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCACACTGTGCAG 1518

Qy       1748 ATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGG 1807
              ||||||||   |||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1519 ATGTCAGTNNNGAGCACTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGG 1578

Qy       1808 AGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGACCCCTTTG 1867
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1579 AGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGACCCCTTTG 1638

Qy       1868 CGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAATCACAG 1927
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Qy       1928 ACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGG 1987
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Db       1699 ACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGG 1758

Qy       1988 ATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTT 2047
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Db       1759 ATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCANGAAGTGGTTT 1818

Qy       2048 CAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAG 2107
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Db       1819 CAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAG 1878

Qy       2108 GGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTA 2167
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Db       1879 GGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTA 1938

Qy       2168 AACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGC 2227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 AACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGC 1998

Qy       2228 CCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCA 2287
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Db       1999 CCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCA 2058

Qy       2288 AAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCC 2347
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Db       2059 AAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCC 2118

Qy       2348 TAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCAC 2407
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Db       2119 TAGAGAGTGAACGAGAAACCATCACTTTCTTTGCACAAGAGGACAGCACTTTCCCTGCAC 2178

Qy       2408 AGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACAT 2467
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Db       2179 AGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACAT 2238

Qy       2468 TTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCA 2527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 TTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCA 2298

Qy       2528 ACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGT 2587
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Db       2299 ACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGT 2358

Qy       2588 GGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGA 2647
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Db       2359 GGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGA 2418

Qy       2648 TTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAAGCCGACT 2707
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Db       2419 TTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAAGCCGACT 2478

Qy       2708 TCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db       2479 TCAACTACAGCAGGCAAAATGGACTCTAG 2507
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RESULT 3
AY401471
LOCUS       AY401471               2775 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM0901 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401471
VERSION     AY401471.1  GI:39757460
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2775)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2775)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2775
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                     /mol_type="genomic DNA"
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     gene            <1. .>2775
                     /locus_tag="HCM0901"
ORIGIN

  Query Match           65.6%;  Score 1796;  DB 9;  Length 2775;
  Best Local Similarity  79.2%;  Pred. No. 0;
  Matches 2222;  Conservative    0;  Mismatches  340;  Indels  243;  Gaps    3;

Qy        100 CGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTG 159
              | |||| | ||      | |||   |||||||| || |||||||| || ||||| || |||
Db         46 CCAGGAGCCGATGGCAGTGAAATTCTTCCCGACTCTATCCCATCTGCCCCTGGAACGCTG 105

Qy        160 CCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTC 219
              |||||||||| |||||||| || ||||| || || ||||||||||||| |||||||||
Db        106 CCTCATTTCATCGAGGAGCCCGAAGATGCATACATCATCAAGAGCAACCCGATTGCACTC 165

Qy        220 AGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCAT 279
              |||||||||| |||||||||||||||| ||||||||||||| || ||||||||||||
Db        166 AGGTGCAAAGCAAGGCCAGCCATGCAGATCTTCTTCAAATGCAATGGGGAGTGGGTCCAT 225

Qy        280 CAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAA 339
              ||||| || || || || || |||| |||| |||||||||| |||||||||| |||
Db        226 CAGAATGAACATGTGTCCGAGGAGAGCCTGGATGAGAGCTCAGGCTTGAAGGTCCGGGAA 285

Qy        340 GTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGG 399
              ||||| |||||||| || ||||| || |||||||||||||||||||| |||||||| |||
Db        286 GTGTTTATCAATGTCACCAGGCAGCAAGTGGAGGACTTCCATGGGCCAGAGGACTACTGG 345

Qy        400 TGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGC 459
              |||||||||| |||||||||||||||| || |||||||| |||||||| ||||||||
Db        346 TGCCAGTGTGTAGCGTGGAGCCACCTGGGAACGTCCAAGAGTAGGAAGGCATCTGTGCGC 405

Qy        460 ATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAA 519
              |||||||||||||||||||||||||||||||| |||||||| ||||| ||||| ||||||
Db        406 ATAGCCTATTTACGGAAAAACTTTGAACAAGATCCACAAGGCAGGGAGGTTCCTATTGAA 465

Qy        520 GGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGG 579
              |||||||| || ||||| || ||||| |||||||||| || || || ||||||||||||
Db        466 GGCATGATCGTGCTGCATTGTCGCCCGCCAGAGGGAGTTCCAGCAGCAGAGGTGGAATGG 525

Qy        580 CTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGAC 639
              |||||||||| |||||||| ||||| ||||| || |||||||||||||||||||||||||
Db        526 CTGAAAAATGAGGAGCCCATCGACTCCGAACAGGATGAGAACATTGACACCAGGGCTGAC 585

Qy        640 CATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCA 699
              |||||| |||||||||| ||||| ||||| || |||||||| |||||||||| ||||||
Db        586 CATAACTTGATCATCAGACAGGCCCGGCTGTCAGACTCAGGGAATTACACCTGTATGGCA 645

Qy        700 GCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC--------- 750
              |||||||||||||| |||||||| ||||| || || ||||| |||||||||
Db        646 GCCAACATCGTGGCCAAGAGGAGGAGCCTCTCAGCAACTGTGGTGGTCTACGTGAATGGA 705

Qy        751 ------------------------------------------------------------ 750

Db        706 GGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAG 765

Qy        751 ------------------------------------------------------------ 750

Db        766 AAACGTTCCCGGACCTGCACCAACCCCGCTCCTCTCAATGGTGGGGCCTTTTGTGAGGGA 825

Qy        751 -----------------------------------GTGGATGGGAGCTGGGAAGTG 771
                                                  |||||||| ||||||||||||
Db        826 ATGTCAGTGCAGAAAATAACCTGCACTGCTCTTTGTCCTGTGGATGGCAGCTGGGAAGTG 885

Qy        772 TGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACA 831
              ||||| |||||||| |||||||||||||||| | || ||||| ||||||||||||||||
Db        886 TGGAGTGAATGGTCAGTCTGCAGCCCAGAGTGTGAACATCTTCGTATCCGTGAGTGCACA 945

Qy        832 GCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAAC 891
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Db        946 GCTCCACCCCCAAGAAATGGGGGCAAGTTCTGTGAAGGTCTCAGCCAGGAATCTGAAAAC 1005

Qy        892 TGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGC 951
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Db       1006 TGCACAGATGGTCTCTGCATTCTAG--------------------------------GC 1032

Qy        952 ATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTT 1011
              |||||||||||||||||||||||||||||||| |||||||||| ||||| || || |||
Db       1033 ATTGAGAATGCCAGCGACATTGCTTTGTACTCCGGCTTGGGTGCAGCCGTGGTAGCTGTT 1092

Qy       1012 GCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGAC 1071
              || |||||||||||||||||||||||||| |||||||||||| |||||||| || |||||
Db       1093 GCGGTCCTGGTCATTGGTGTCACCCTCTACAGACGGAGCCACAGTGACTACGGAGTGGAT 1152

Qy       1072 GTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGT 1131
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1153 GTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTTCGT 1212

Qy       1132 CAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTC 1191
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Qy       1192 CTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGT 1251
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Qy       1252 CTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCG 1311
              |||||||| || || |||||||||||||||||||||||||||||| || ||||| ||
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Qy       1312 GACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCT 1371
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Qy       1372 GAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGT 1431
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Qy       1432 ACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGG 1491
              ||||| |||||||||| |||| ||| |||||||||||||||||||||| || ||||||
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Qy       1492 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAAT 1551
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Qy       1552 ACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATT 1611
              ||||
Db       1591 ACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1650

Qy       1612 TATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTG 1671
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Db       1651 NNNNNNNNNNNNNNNNNNNNNNNNNNNNCCTGCAGTCAGATGGATCTGAGGTTCTCCTG 1710

Qy       1672 AGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACC 1731
              |||||||||||||||||||| |||||||| ||| | ||||| |||||||||| |||||
Db       1711 AGTCCTGAAGTCACCTGTGGGCCTCCAGATATGCTTGTCACAACTCCCTTTGCGCTGACC 1770

Qy       1732 ATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACA 1791
              ||||| |||||||||| |||||||| ||||| ||||| || ||  | ||||||||||
Db       1771 ATCCCTCACTGTGCAGACGTCAGTTCAGAGCACTGGAACATTCACCTGAAGAAGAGGACC 1830

Qy       1792 CAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGC 1851
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Qy       1912 GGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATG 1971
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Qy       2572 GTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCC 2631

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RESULT 4
AK018177
LOCUS       AK018177               3866 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
            enriched library, clone:6330415E02 product:TRANSMEMBRANE RECEPTOR
            UNC5H2 homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK018177
VERSION     AK018177.1  GI:12857775
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3866)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 10.0 and subtraction to
            Rot = 100.0. Second strand cDNA was prepared with the primer
            adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
            bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
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                     /db_xref="GI:12857776"
                     /translation="MRARSGVRSALLLALLLCWDPTPSLAGVDSAGQVLPDSYPSAPA
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                     AKEVPLDHEVLLQCRPPEGVPVAEVEWLKNEDVIDPAQDTNFLLTIDHNLIIRQARLS
                     DTANYTCVAKNIVAKRRSTAATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNP
                     APLNGGAFCEGQAFQKTACTTVCPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNG
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ORIGIN

  Query Match           20.7%;  Score 565.8;  DB 3;  Length 3866;
  Best Local Similarity  54.2%;  Pred. No. 8.1e-154;
  Matches 1541;  Conservative    0;  Mismatches 1057;  Indels  243;  Gaps   10;

Qy         25 GGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGGCTGGGGCTGTGCTTCTGGGCGGCA 84
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Qy         85 GGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCA 144
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Qy        145 GCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGC 204
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Qy        385 CCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGG 444
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Qy        505 GAAGTTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCT 564
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Qy        625 GACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAAT 684
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Qy       1867 GCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAATCACA 1926
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Qy       1927 GACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTG 1986
Db       2481 CGCTCTGCAGTCAAGCGGCTCCAGCTGGCCATCTTCGCCCCAGCCCTCTGCACCTCCCTG 2540

Qy       1987 GATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTT 2046
Db       2541 GAGTATAGCCTCAGGGTCTACTGTCTGGAGGACACACCTGTAGCACTGAAGGAGGTCCTG 2600

Qy       2047 TCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAA 2106
Db       2601 GAGCTGGAGAGGACTCTGGGTGGCTACTTGGTGGAGGAGCCCAAGCCTTTGCTCTTTAAG 2660

Qy       2107 GGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATT 2166
Db       2661 GACAGTTACCACAACCTACGCCTCTCCCTCCATGACATCCCCCATGCCCACTGGAGGAGC 2720

Qy       2167 AAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAG 2226
Db       2721 AAACTACTGGCCAAGTACCAGGAGATTCCCTTCTACCACGTCTGGAATGGCAGCCAGAGA 2780

Qy       2227 CCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGC 2286
Db       2781 GCCCTGCACTGCACTTTCACCCTGGAGAGGCATAGCCTGGCCTCCACGGAGTTCACCTGT 2840

Qy       2287 AAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATC 2346
Db       2841 AAGGTCTGCGTGCGGCAGGTCGAAGGGGAAGGCCAGATTTTCCAGCTGCACACAACGTTG 2900

Qy       2347 CTAGAGAGTGAACGAGAAACCAT---CACTTTCTTCGCACAAGAGGACAGCACTTTCCCT 2403
Db       2901 GCCGAGACGCCTGCTGGCTCCCTGGATGCTCTCTGCTCTGCCCCGGGCAATGCCATCACC 2960

Qy       2404 GCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCT 2463
Db       2961 ACCCAGCTGGGACCCTATGCCTTCAAGATACCCCTGTCCATCCGCCAAAAGATCTGCAGC 3020

Qy       2464 ACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGC 2523
Db       3021 AGCCTGGACGCCCCCGACTCCCGGGGCAACGACTGGAGGCTGTTGGCGCAGAAGCTGTCC 3080

Qy       2524 ATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAAC 2583
Db       3081 ATGGACCGGTACCTAAACTACTTCGCCACCAAAGCTAGTCCCACAGGTGTCATCTTAGAC 3140

Qy       2584 CTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAA 2643
Db       3141 CTCTGGGAAGCTCGGCAACAGGATGACGGGGACCTCAACAGCCTGGCCAGTGCCTTGGAG 3200

Qy       2644 GAGATTGGGAGGACACACACG 2664
Db       3201 GAGATGGGCAAGAGTGAGATG 3221
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RESULT 5
CD636011
LOCUS CD636011 532 bp mRNA linear EST 12-JAN-2004
DEFINITION 56033904H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD636011
VERSION CD636011.1 GI:40284278
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 532)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES Location/Qualifiers
source 1. .532
/organism="Homo sapiens"
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/clone_lib="FLP"
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ORIGIN

Query Match 19.3%; Score 529.4; DB 6; Length 532;
Best Local Similarity 99.8%; Pred. No. 1.9e-143;
Matches 530; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1151 AACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGC 1210
Db          1 AACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGC 60

Qy       1211 CAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACA 1270
Db         61 CAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACA 120

Qy       1271 AGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCC 1330
Db        121 AGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCC 180

Qy       1331 AGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATC 1390
Db        181 AGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATC 240

Qy       1391 ATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 1450
Db        241 ATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 300

Qy       1451 AAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTG 1510
Db        301 AAATGCCCTACATCCAAAATCAGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTG 360

Qy       1511 GTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCA 1570
Db        361 GTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCA 420
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Qy       1571 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG 1630
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Db        421 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG 480

Qy       1631 GTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1681
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Db        481 GTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 531


RESULT 6
CD636014/c
LOCUS       CD636014                596 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56033928J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD636014
VERSION     CD636014.1  GI:40284281
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .596
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
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ORIGIN

  Query Match             19.3%;  Score 529.4;  DB 6;  Length 596;
  Best Local Similarity   93.1%;  Pred. No. 2e-143;
  Matches  593;  Conservative    0;  Mismatches    1;  Indels   43;  Gaps    2;

Qy       1046 GGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCC 1105
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Db        595 GGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCC 536

Qy       1106 AGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAG 1165
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Db        535 AGACCTTCAACTTCAAAACAGTCCGTCAA------------------------------ 507

Qy       1166 AAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGA 1225
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 -----------GGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGA 458

Qy       1226 GCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAG 1285
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Db        457 GCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGGGCTCATGACAG 398

Qy       1286 AGTCCTCAC-TCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATG 1344
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Db        397 AGTCCTCACGTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATG 338

Qy       1345 GTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTT 1404
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Db        337 GTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTT 278

Qy       1405 CCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATC 1464
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Db        277 CCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATC 218

Qy       1465 CAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCAT 1524
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Db        217 CAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCAT 158

Qy       1525 TTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCC 1584
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Db        157 TTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCC 98

Qy       1585 ATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTC 1644
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          97 ATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTC 38

Qy       1645 CAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1681
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Db          37 CAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1


RESULT 7
CD636012/c
LOCUS       CD636012                530 bp    mRNA    linear   EST 12-JAN-2004
DEFINITION  56033904J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD636012
VERSION     CD636012.1  GI:40284279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.
FEATURES             Location/Qualifiers
     source          1. .530
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ORIGIN

  Query Match             18.9%;  Score 517.4;  DB 6;  Length 530;
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  Matches  529;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1151 AACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGC 1210
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Db        530 AACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGC 471

Qy       1211 CAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACA 1270
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Db        470 CAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCTCTGGACA 411

Qy       1271 AGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCC 1330
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Db        410 AGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCC 351

Qy       1331 AGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATC 1390
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Db        350 AGAGCTCGTTCATGGTTT-CCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATC 292

Qy       1391 ATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 1450
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Db        291 ATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 232

Qy       1451 AAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTG 1510
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        231 AAATGCCCTACATCCAAAATCAGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTG 172
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Qy       1511 GTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCA 1570
Db        171 GTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCA 112

Qy       1571 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG 1630
Db        111 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG 52

Qy       1631 GTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAG 1681
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RESULT 8
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LOCUS       AY406491                2802 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406491
VERSION     AY406491.1  GI:39762465
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2802)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2802)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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ORIGIN

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Qy         46 CGCTGGCTCCCGTGGCTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGA 105
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Qy        106 ACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAG---CTCCTGGGACACTGCCT 162
Db        127 GATGACTTTTTCATGAACTCCCAGAAACTTTTCCTTCTGATCCACCTGAGCCTCTGCCA 186

Qy        163 CATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGG 222
Db        187 CATTTCCTTATTGAGCCTGAAGAAGCTTATATTGTGAAGAATAAGCCTGTGAACCTGTAC 246

Qy        223 TGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAG 282
Db        247 TGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAAGTGTAATAGTGAATGGGTTCATCAG 306

Qy        283 AACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTG 342
Db        307 AAGGACCACATAGTAGATGAAAGAGTAGATGAAACTTCCGGTCTCATTGTCCGGGAAGTG 366

Qy        343 TTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGC 402
Db        367 AGCATTGAGATTTCGCGCCAGCAAGTGGAAGAACTCTTTGGACCTGAAGATTACTGGTGC 426

Qy        403 CAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATA 462
Db        427 CAGTGTGTGGCCTGGAGCTCCGCGGGTACCACAAAGAGCCGGAAGGCGTATGTGCGCATT 486

Qy        463 GCCT------ATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATT 516
Db        487 GCATNNNNNNNNNNNCGGAAGACATTTGAGCAGGAACCCCTAGGAAAGGAAGTGTCTTTG 546

Qy        517 GAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAA 576
Db        547 GAACAGGAAGTCTTACTCCAGTGTCGACCACCTGAAGGGATCCCAGTGGCTGAGGTGGAA 606

Qy        577 TGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCT 636
Db        607 TGGTTGAAAAATGAAGACATAATTGATCCCGTTGAAGATCGGAATTTTTATATTACTATT 666

Qy        637 GACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATG 696
Db        667 GATCACAACCTCATCATAAAGCAGGCCCGACTCTCTGATACTGCAAATTACACCTGTGTT 726

Qy        697 GCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGAT 756
Db        727 GCCAAAAACATTGTTGCCAAGAGGAAAAGTACAACTGCCACTGTCATAGTCTATGTCAAC 786

Qy        757 GGGAGCTGGGAAGTGTGGAGCGAATGGTCCGT---------CTGCAGTCCAGAGTGTGAA 807
Db        787 GGTGGCTGGTCCACCTGGACGGAGTGGTCTGTGTGTAACAGCCGCTGTGGACGAGGGTAT 846

Qy        808 CATTTGCGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGCAAATTCTGTGAA 867
Db        847 CAGAAACGTACAAGGACTTGTACCAACCCGGCACCACTCAATGGGGGTGCCTTCTGTGAA 906

Qy        868 GGTCTAAGCCAGGA------------------ATCTGAAAACTGCACAGATGGTCTTTG 908
Db        907 GGGCAGAGTGTGCAGAAAATAGCCTGTACTACGTTATGCCCAGTGGATGGCAGGTGGACG 966

Qy        909 CATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCGA 968
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Qy        969 CATTGCTTTGTACTCGGGCTTGGGTGC--------TGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db       1027 ACGGCGCCAGCCCCCAAGAATGGAGGCAAGGACTGCGACGGCCTCGTCTTGCAATCCAAG 1086

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACT---ATGGCGTGGACGTCATT 1077
Db       1087 AACTGCACTGATGGGCTTTGCATGCAGACTGCTCCTGATTCAGATGATGTTGCTCTCTAT 1146

Qy       1078 GACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCC 1137
Db       1147 GTTGGGATTGTGATAGCAGTGATCGTTTGCCTGGCGATCTCTGTAGTTGTGGCCTTGTTT 1206

Qy       1138 AAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAAT 1197
Db       1207 GTGTATCGGAAGAATCATCGTGACTTTGAGTCAGATATTATTGACTCTTCGGCACTCAAT 1266

Qy       1198 TCTGCCATGCAGCCAG----------------ATCTGACAGTGAGCCGGACATACAGCGG 1241
Db       1267 GGGGGCTTTCAGCCTGTGAACATCAAGGCAGCAAGACAAGATCTGCTGGCTGTACCCCCA 1326

Qy       1242 ACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCT--------CATGACAGAGTCCTCA 1293
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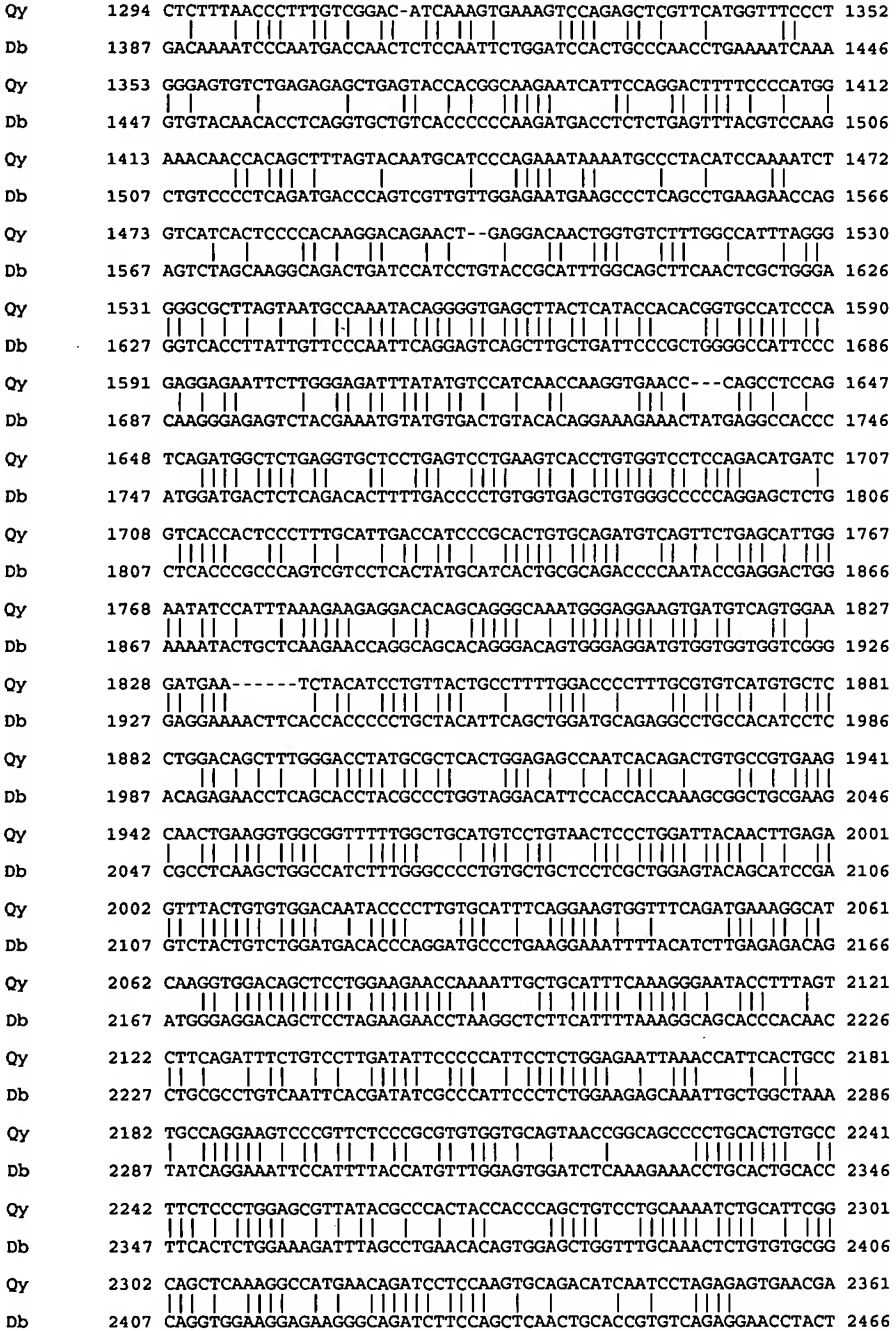

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Qy       1353 GGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGG 1412
Db       1447 GTGTACAACACCTCAGGTGCTGTCACCCCCCAAGATGACCTCTCTGAGTTTACGTCCAAG 1506

Qy       1413 AAACAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCT 1472
Db       1507 CTGTCCCCTCAGATGACCCAGTCGTTGTTGGAGAATGAAGCCCTCAGCCTGAAGAACCAG 1566

Qy       1473 GTCATCACTCCCCACAAGGACAGAACT--GAGGACAACTGGTGTCTTTGGCCATTTAGGG 1530
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Qy       1531 GGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCA 1590
Db       1627 GGTCACCTTATTGTTCCCAATTCAGGAGTCAGCTTGCTGATTCCCGCTGGGGCCATTCCC 1686

Qy       1591 GAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACC---CAGCCTCCAG 1647
Db       1687 CAAGGGAGAGTCTACGAAATGTATGTGACTGTACACAGGAAAGAAACTATGAGGCCACCC 1746

Qy       1648 TCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATC 1707
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Qy       1708 GTCACCACTCCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGG 1767
Db       1807 CTCACCCGCCCAGTCGTCCTCACTATGCATCACTGCGCAGACCCCAATACCGAGGACTGG 1866

Qy       1768 AATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAA 1827
Db       1867 AAAATACTGCTCAAGAACCAGGCAGCACAGGGACAGTGGGAGGATGTGGTGGTGGTCGGG 1926

Qy       1828 GATGAA------TCTACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTC 1881
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Qy       1882 CTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAG 1941
Db       1987 ACAGAGAACCTCAGCACCTACGCCCTGGTAGGACATTCCACCACCAAAGCGGCTGCGAAG 2046

Qy       1942 CAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGA 2001
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Qy       2002 GTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCAT 2061
Db       2107 GTCTACTGTCTGGATGACACCCAGGATGCCCTGAAGGAAATTTTACATCTTGAGAGACAG 2166

Qy       2062 CAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGT 2121
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Qy       2482 GCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCT 2541
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ACCESSION AY411747
VERSION AY411747.1 GI:39767715
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Matches 1380; Conservative 0; Mismatches 909; Indels 243; Gaps 10;

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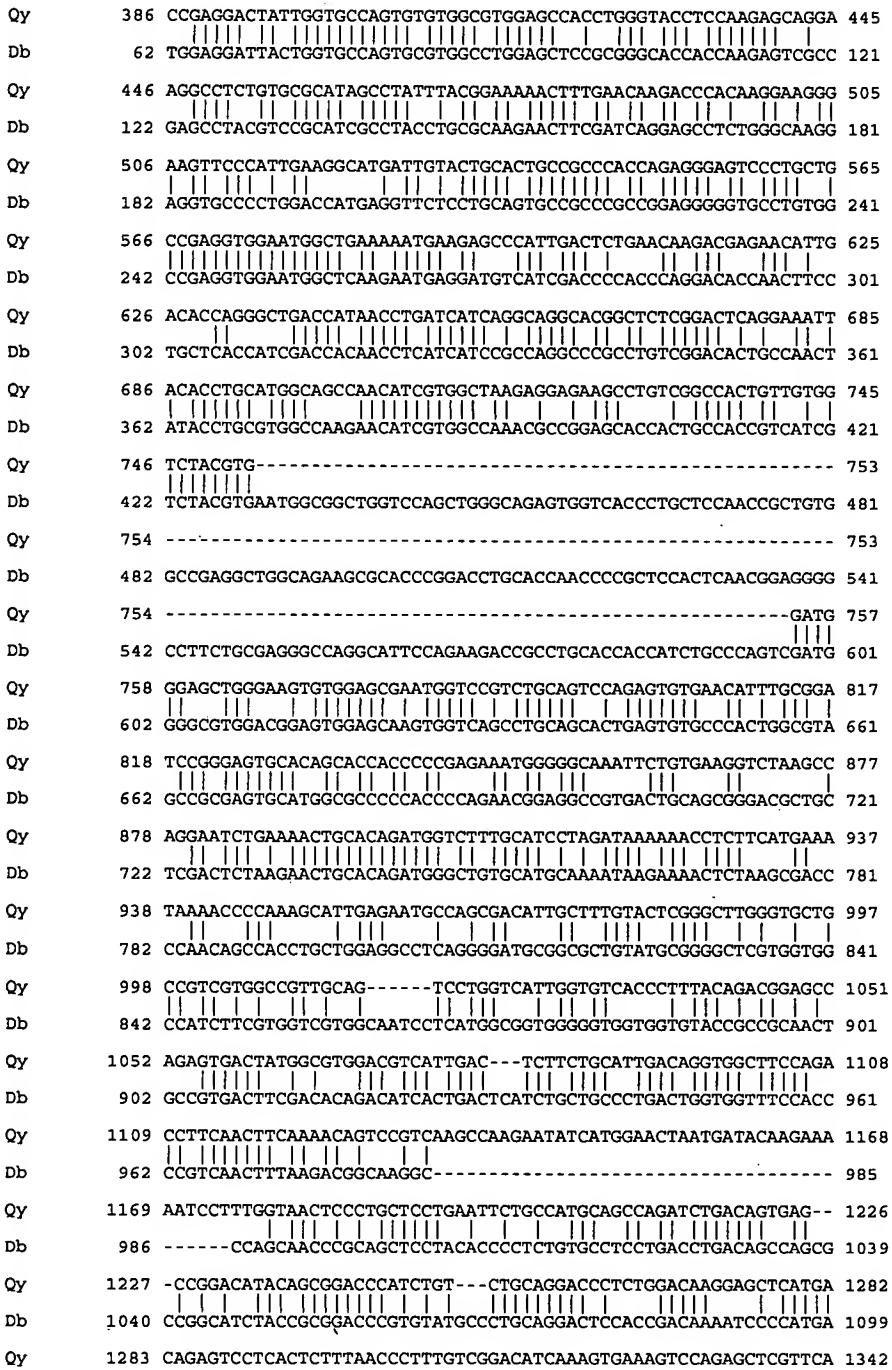

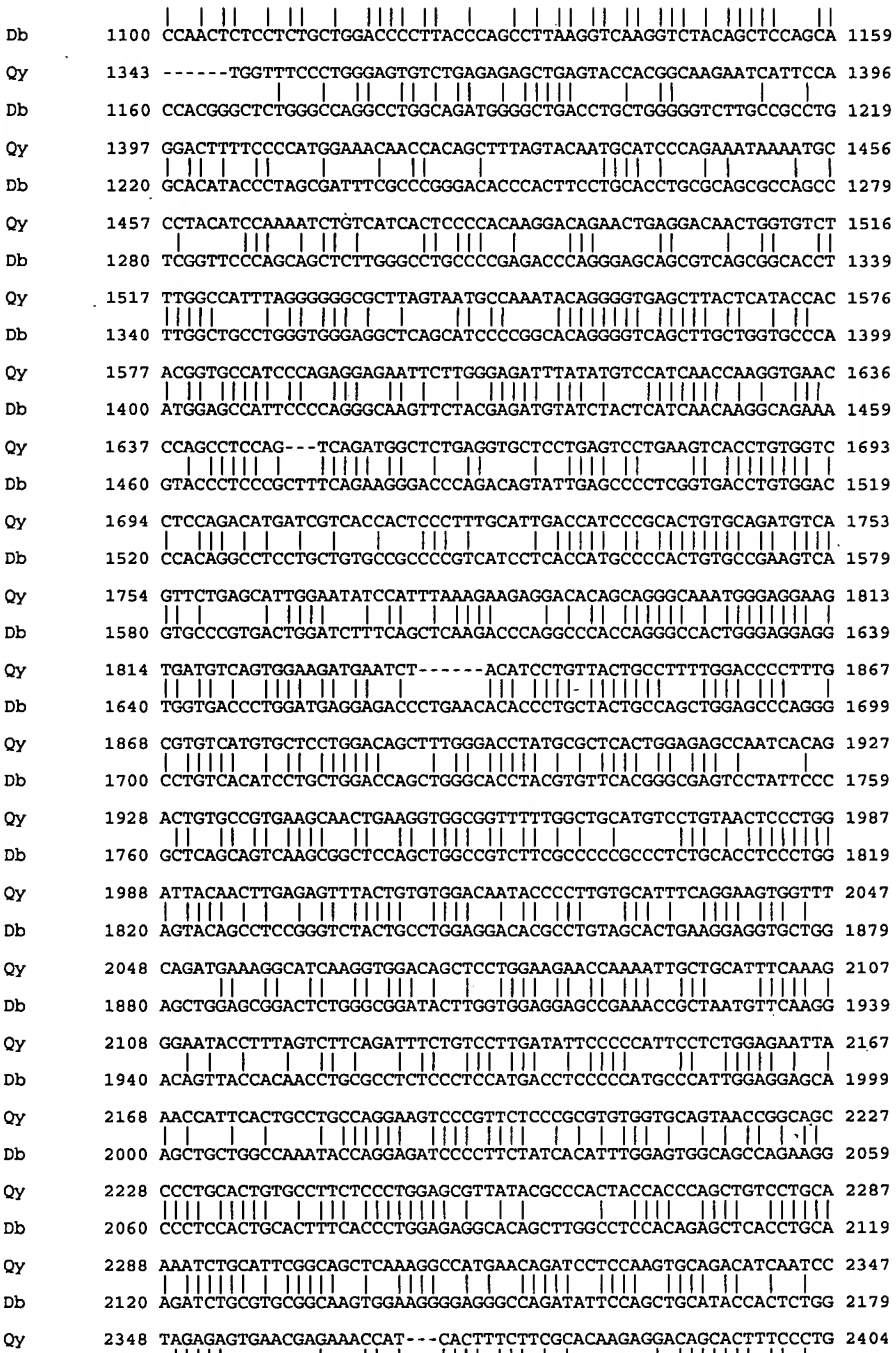

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Db       2480 AGATGGGCAAGA 2491
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DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.
ACCESSION AK031655
VERSION AK031655.1 GI:26327502
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3790)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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ORIGIN

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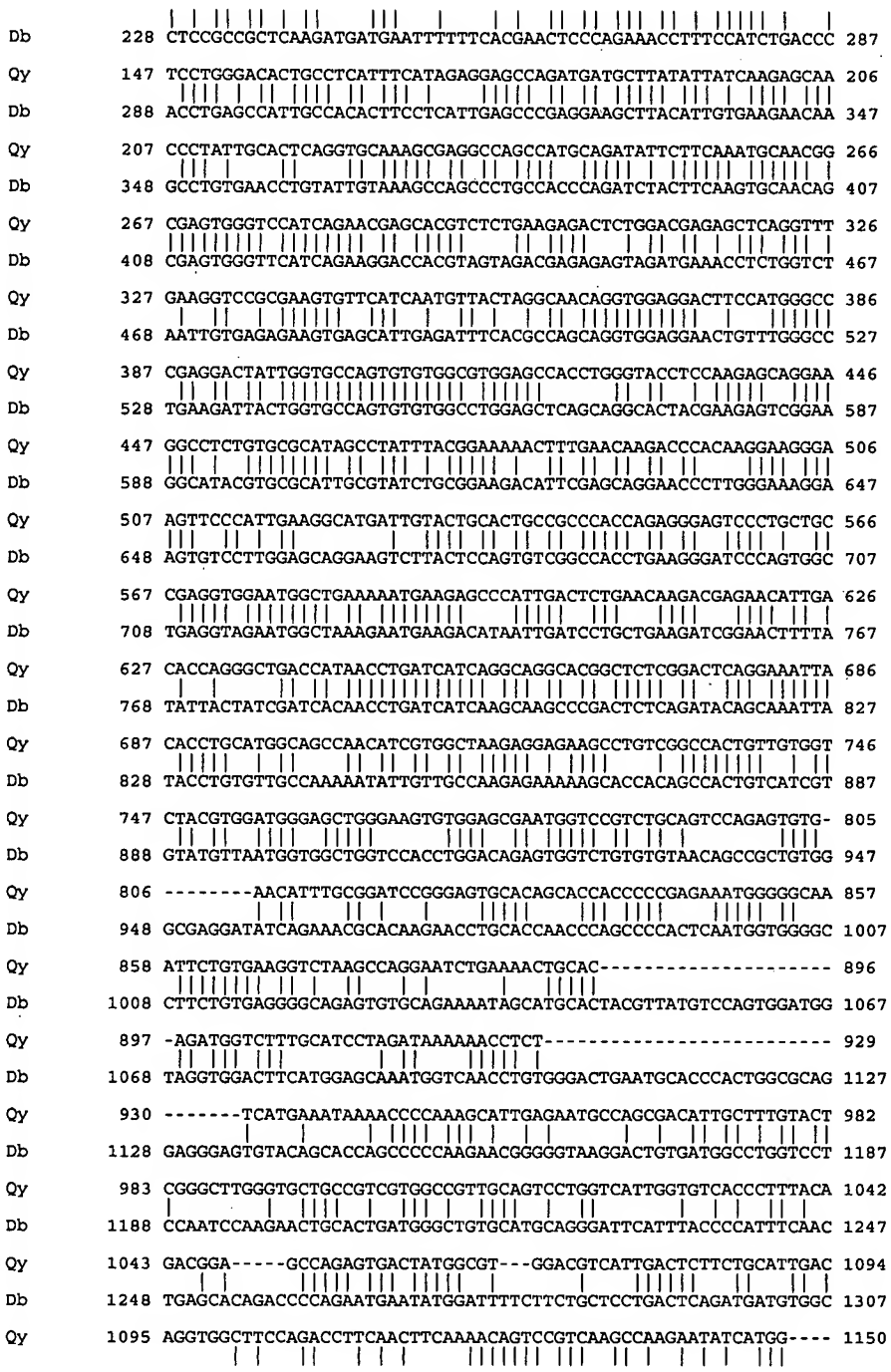
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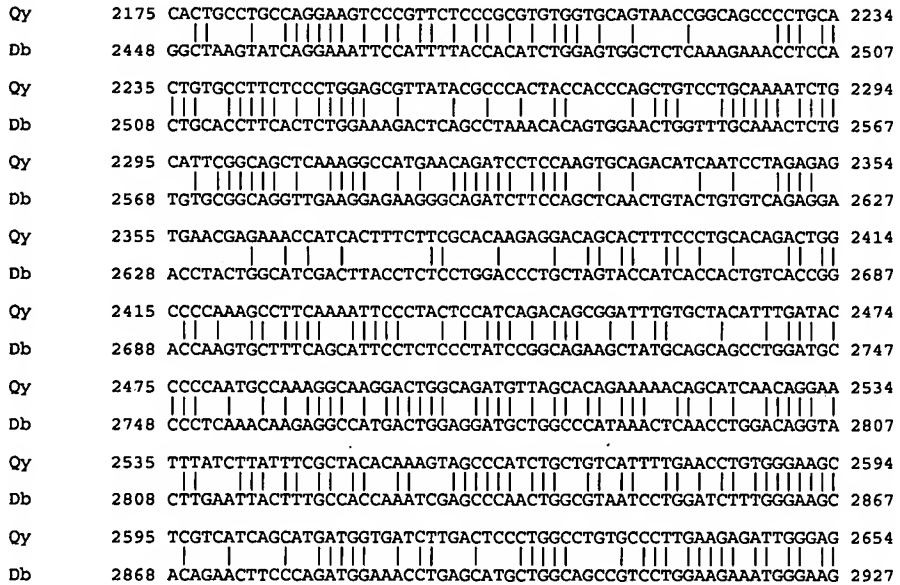

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ACCESSION AY406493
VERSION AY406493.1 GI:39762467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2791)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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ORIGIN

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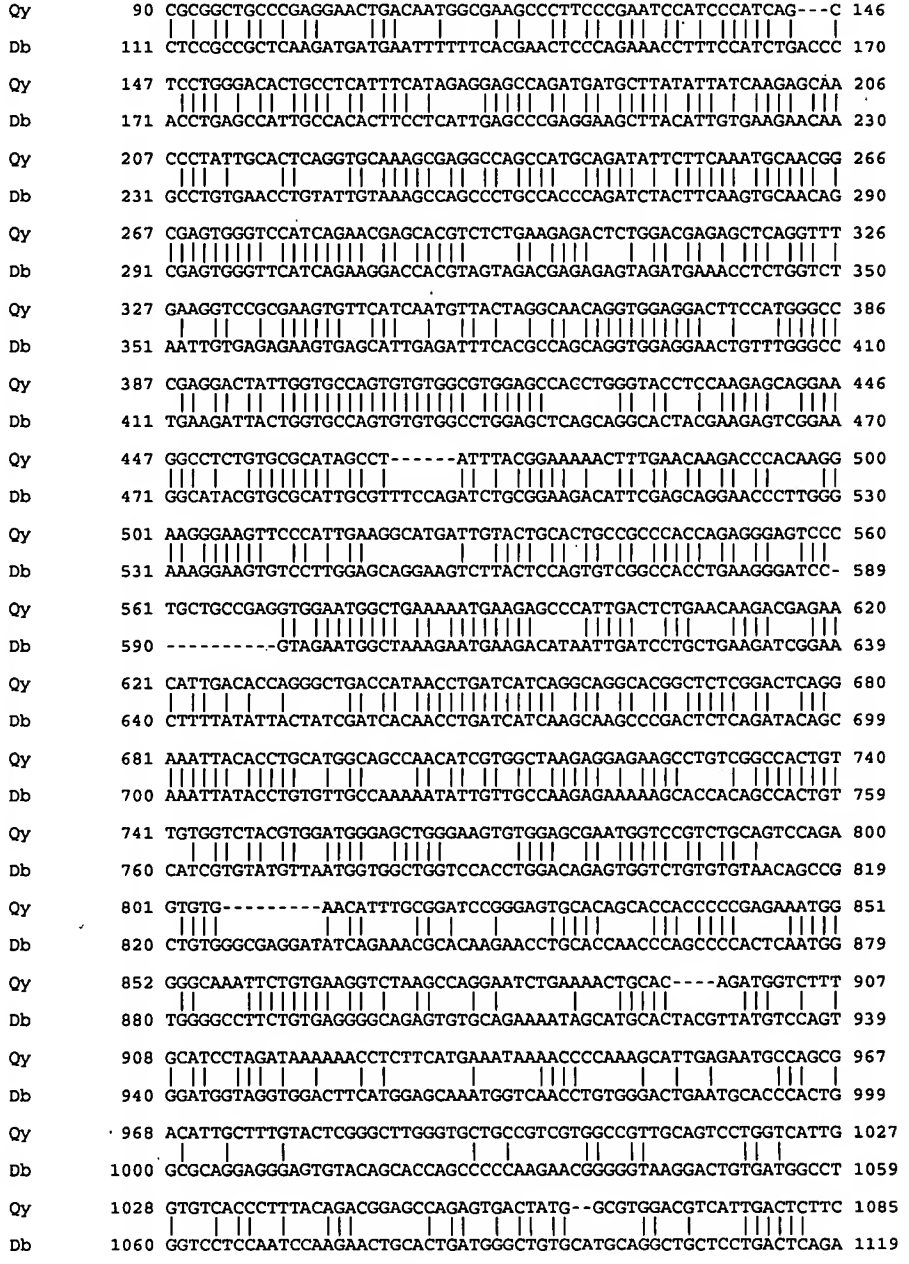
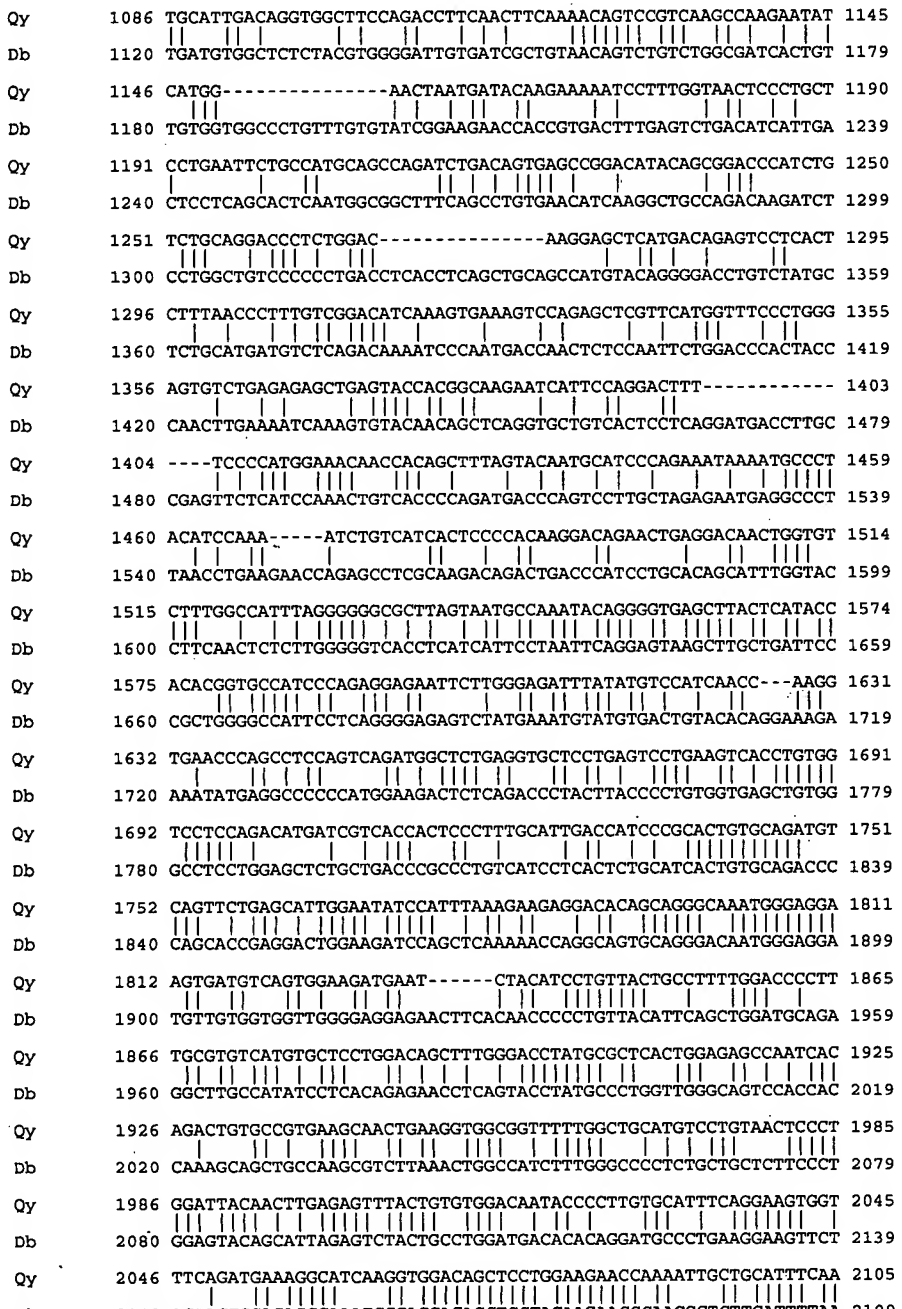
Matches 1403; Conservative 0; Mismatches 1188; Indels 95; Gaps 12;





RESULT 12
AY411749
LOCUS AY411749 2532 bp DNA linear GSS 12-DEC-2003
DEFINITION Mus musculus HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY411749
VERSION AY411749.1 GI:39767717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2532)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers

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                     /db_xref="taxon:10090"
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ORIGIN
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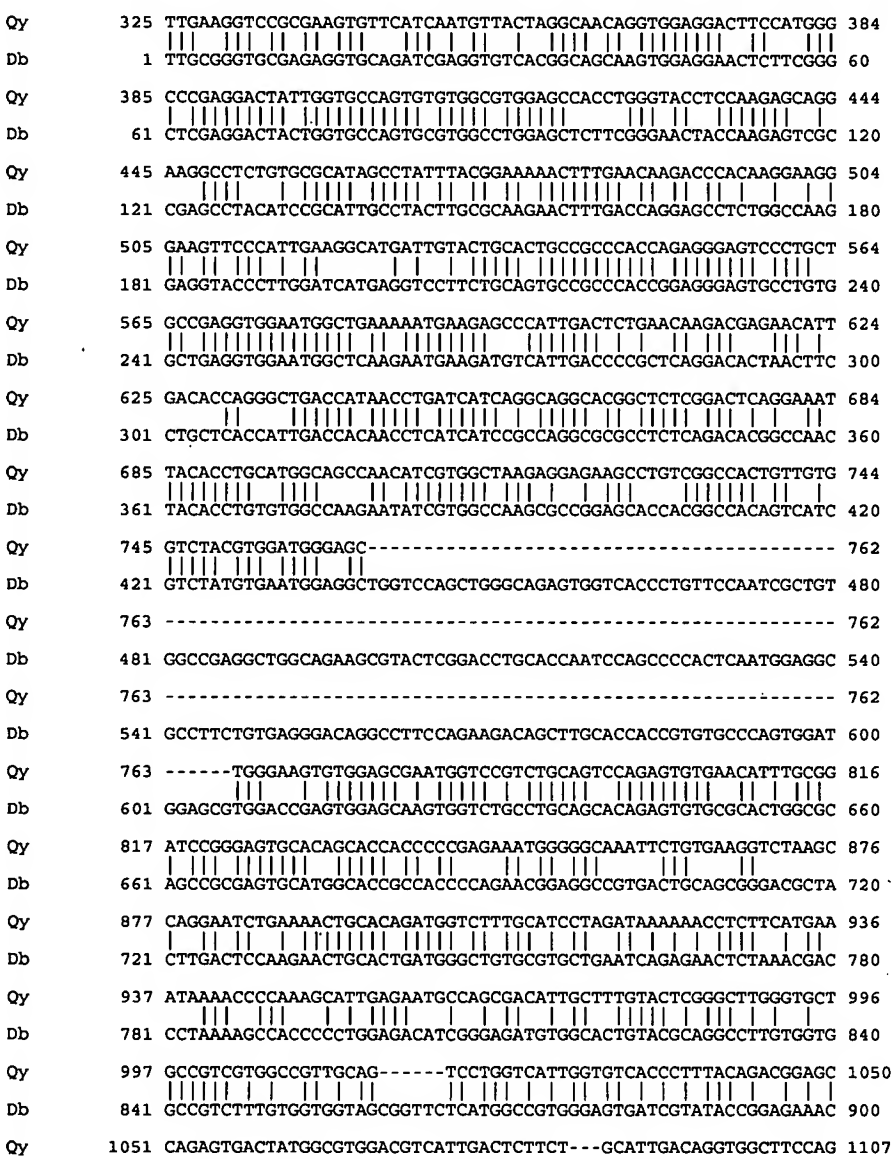
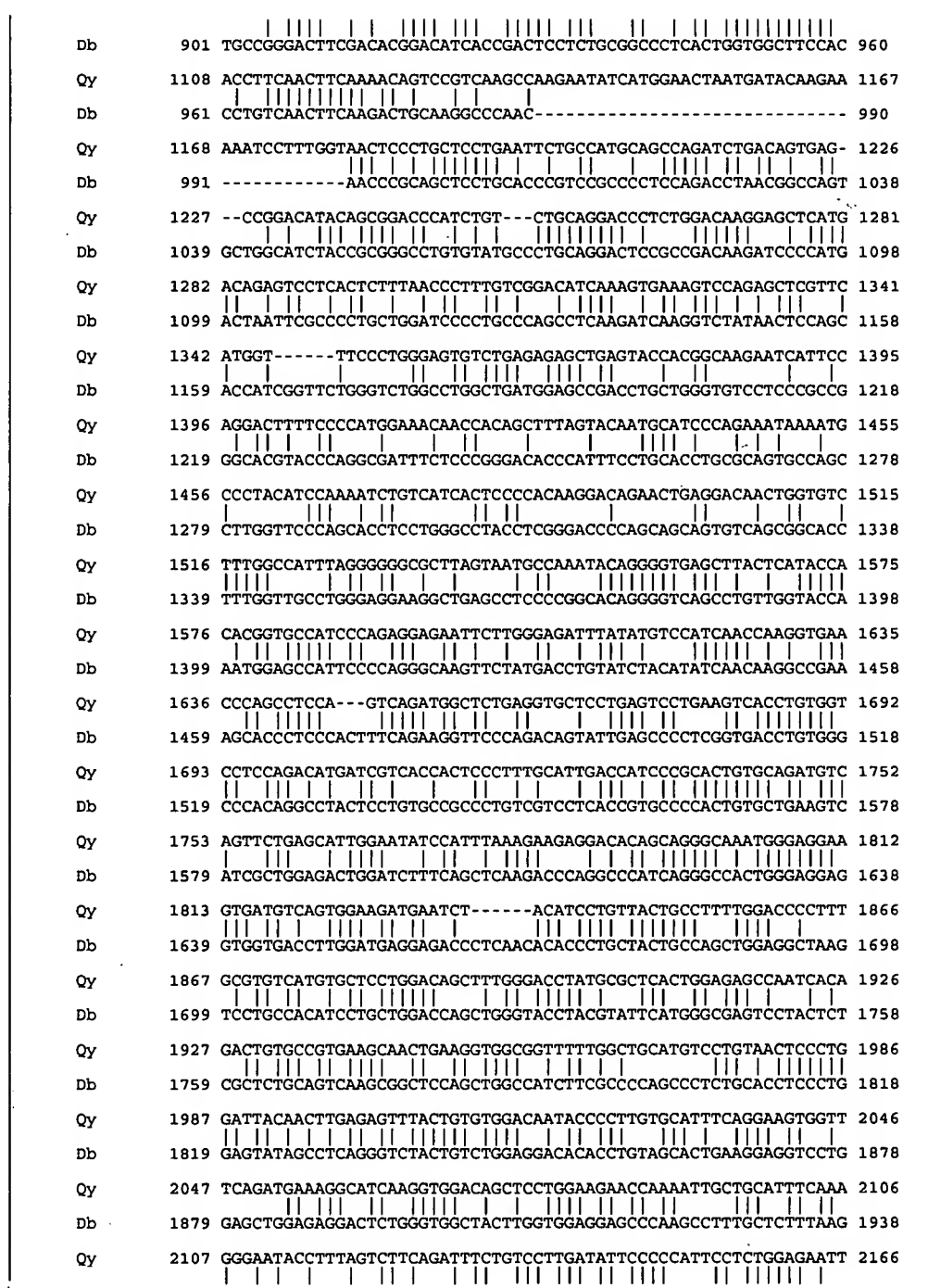
Query Match 17.2%; Score 471.8; DB 9; Length 2532;
Best Local Similarity 54.0%; Pred. No. 2.9e-126;
Matches 1368; Conservative 0; Mismatches 922; Indels 243; Gaps 10;





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Db       1939 GACAGTTACCACAACCTACGCCTCTCCCTCCATGACATCCCCCATGCCCACTGGAGGAGC 1998

Qy       2167 AAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAG 2226

Db       1999 AAACTACTGGCCAAGTACCAGGAGATTCCCTTCTACCACGTCTGGAATGGCAGCCAGAGA 2058

Qy       2227 CCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGC 2286

Db       2059 GCCCTGCACTGCACTTTCACCCTGGAGAGGCATAGCCTGGCCTCCACGGAGTTCACCTGT 2118

Qy       2287 AAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATC 2346

Db       2119 AAGGTCTGCGTGCGGCAGGTCGAAGGGGAAGGCCAGATTTTCCAGCTGCACACAACGTTG 2178

Qy       2347 CTAGAGAGTGAACGAGAAACCAT---CACTTTCTTCGCACAAGAGGACAGCACTTTCCCT 2403

Db       2179 GCCGAGACGCCTGCTGGCTCCCTGGATGCTCTCTGCTCTGCCCCGGGCAATGCCATCACC 2238

Qy       2404 GCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCT 2463

Db       2239 ACCCAGCTGGGACCCTATGCCTTCAAGATACCCCTGTCCATCCGCCAAAAGATCTGCAGC 2298

Qy       2464 ACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGC 2523

Db       2299 AGCCTGGACGCCCCCAACTCCCGGGGCAACGACTGGAGGCTGTTGGCGCAGAAGCTGTCC 2358

Qy       2524 ATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAAC 2583

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Qy       2584 CTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAA 2643

Db       2419 CTCTGGGAAGCTCGGCAACAGGATGACGGGGACCTCAACAGCCTGGCCAGTGCCTTGGAG 2478

Qy       2644 GAGATTGGGAGGA 2656

Db       2479 GAGATGGGCAAGA 2491


RESULT 13
BX915627/c
LOCUS       BX915627                812 bp    mRNA    linear   EST 07-MAY-2004
DEFINITION  BX915627 Sus Scrofa library (scan) Sus scrofa cDNA clone
            scan0030d.c.10 5prim, mRNA sequence.
ACCESSION   BX915627
VERSION     BX915627.1  GI:41132406
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
            Soares,M., Bonaldo,F. and Hatey,F.
  TITLE     A Pig Normalised Multi-Tissue cDNA Library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tosser-Klopp G
            Genetique Animale
            Institut National de la Recherche Agronomique
            Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
            cedex, FRANCE
            Tel: 33 (0) 5.61.28.51.14
            Fax: 33 (0) 5.61.28.53.08
            Email: tosser@toulouse.inra.fr
            Sequence cleaned of vector, adaptator and repetitions. Contact us
            at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0030  row: c  column: 10.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /dev_stage="from embryos to adults"
                     /clone_lib="Sus Scrofa library (scan)"
                     /note="tissues: adipose tissue, brain, kidney, liver,
                     muscle, ovary, testis, heart, hypothalamus, pancreas,
                     skin, spleen, thymus, placenta, pituitary gland, seminal
                     vesicle, small intestine, uterus, adrenals, bulbo uretral
                     gland, cerebral trunk, epididymis, female gonad,
                     gall-bladder, hippocampus, large intestine, male gonad,
                     melanocytes, stomach, udder"
ORIGIN

  Query Match             16.1%;  Score 440;  DB 5;  Length 812;
  Best Local Similarity   73.4%;  Pred. No. 4.2e-117;
  Matches  661;  Conservative    0;  Mismatches  142;  Indels   97;  Gaps    4;

Qy        553 GGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAA 612

Db        812 GGGGTTCNTGCTGCAGAGTGGGAATGGCTGAAAAACGAGGAGCCCATGNACTCTGACCAA 753

Qy        613 GACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCG 672

Db        752 GATGAGAACA-TGATACCAGGGCAGACCACAACCTCATCATCAGGCAGGCACGGCTCTCG 694

Qy        673 GACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCG 732

Db        693 GATTCAGGGAATTACACCTGCATGGCAGCCAACATCGTGGCCAAGAGGAGGAGCCTGTCG 634

Qy        733 GCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGC 792

Db        633 GCCACAGTGGTGGTTTATGTGAATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGC 574

Qy        793 AGTCCAGAGTGTG---------AACATTTGCGGATCCGGGAGTGCACAGCACCACCCCCG 843

Db        573 AATGTTCGCTGTGGTAGAGGATGGCAGAAACGTTCCCGGACCTGCACCAATCCAGCTCCT 514

Qy        844 AGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGATGGT 903

Db        513 CTCAATGGTGGGGCCTTTTGTGAGGGAATGTCAGTGCAGAAAATAACCTGCAC------T 460

Qy        904 CTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAATGCC 963

Db        459 TCTCTCTGTCCTGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGTATTGAGAACGCC 400

Qy        964 AGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTGGTC 1023

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Qy       1024 ATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGACTCT 1083

Db        339 ATCGGCGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGATGTCATCGACTCT 280

Qy       1084 TCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAGAAT 1143

Db        279 TCTGCATTGACA---------------------------------------------- 268

Qy       1144 ATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCC 1203

Db        267 --------------------------------GGTAACTCCCTGCTTCTGAATCCCTCC 241

Qy       1204 ATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGACCCT 1263

Db        240 ATGCAACCAGACCTAACAGTCAGCCGAACGTACAGTGGGCCCATCTGTCTGCAGGATCCC 181

Qy       1264 CTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTG 1323

Db        180 CTGGACAAGGAACTCATGACGGAGTCGTCACTCTTTAACCCTCTGTCAGACATCAAGGTC 121

Qy       1324 AAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGC 1383

Db        120 AAAGTACAGAGCTCATTCATGGTTTCCCTGGGTGTGTCGGAGAGAGCCGAGTACCATGGC 61
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Qy       1384 AAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCC 1443
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RESULT 14
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LOCUS       AY411748               2532 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY411748
VERSION     AY411748.1  GI:39767716
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /locus_tag="HCM4327"
ORIGIN

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  Matches 1042;  Conservative    0;  Mismatches  821;  Indels   75;  Gaps    9;

Qy        752 TGGATGGGAGCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATT 811
Db        596 TCGATGGGGCGTGGACGGAGTGGAGCAAGTGGTCAGCCTGCAGCACTGAGTGTGCCCACT 655

Qy        812 TGCGGATCCGGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTC 871
Db        656 GGCGTAGCCGCGAGTGCATGGCGCCCCCACCCCAGAACGGAGGCCGTGACTGCAGCGGGA 715

Qy        872 TAAGCCAGGAATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTC 931
Db        716 CGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAAACTCTAA 775

Qy        932 ATGAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGG 991
Db        776 GCGACCCCAACAGCCACCTGCTGGAGGCCTCAGGGGATGCGGCGCTGTATGCGGGGCTCG 835

Qy        992 GTGCTGCCGTCGTGGCCGTTGCAG------TCCTGGTCATTGGTGTCACCCTTTACAGAC 1045
Db        836 TGGTGGCCGTCTTCNTGGTCNTGGCAATCCTCATGGCGGTGGGGGTGGTGGTGTACCGCC 895

Qy       1046 GGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC---TCTTCTGCATTGACAGGTGGCT 1102
Db        896 GCAACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGACTGGTGGTT 955

Qy       1103 TCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATAC 1162
Db        956 TCCACCCCGTCAACTTTAAGACGGCAAGGC---------------------------- 985

Qy       1163 AAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAG 1222
Db        986 ------------CCAGCAACCCGCAGCTCCTACACCCCTCTGTGCCTCCTGACCTGACAG 1033

Qy       1223 TGAG---CCGGACATACAGCGGACCCATCTGT---CTGCAGGACCCTCTGGACAAGGAGC 1276
Db       1034 CCAGCGCCGGCATCTACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGACAAAATCC 1093

Qy       1277 TCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCT 1336
Db       1094 CCATGACCAACTCTCCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCT 1153

Qy       1337 CGTTCA------TGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATC 1390
Db       1154 CCAGCACTACGGGCTCTGGGCCAGGCCTGGCAGATGGGGCTGACCTGCTGGGAGTCTTGC 1213

Qy       1391 ATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCATCCCAGAAATA 1450
Db       1214 CGCCTGGCACATACCCTAGCGATTTCGCCCGGGACACCCACTTCCTGCACCTGCGCAGCG 1273

Qy       1451 AAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTGAGGACAACTG 1510
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Qy       1511 GTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTGAGCTTACTCA 1570
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Qy       1571 TACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCCATCAACCAAG 1630
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Qy       1631 GTGAACCCAGCCTCCAG---TCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAAGTCACCT 1687
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Qy       1688 GTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCATTGACCATCCCGCACTGTGCAG 1747
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Qy       1748 ATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGCAAATGGG 1807
Db       1574 AAGTCAGTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCCACCAGGGCCACTGGG 1633

Qy       1808 AGGAAGTGATGTCAGTGGAAGATGAATC------TACATCCTGTTACTGCCTTTTGGACC 1861
Db       1634 AGGAGGTGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAGC 1693

Qy       1862 CCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCAA 1921
Db       1694 CCAGGGCCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTCACGGGCGAGTCCT 1753

Qy       1922 TCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAACT 1981
Db       1754 ATTCCCNNNNNNCAGTCNNNNNGCTCCNGCTGGCCGTCTTNGCCCCTGCCCTCTGCACCT 1813

Qy       1982 CCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAAG 2041
Db       1814 CCCTGGANNNNNGCCTCCGGGTCTACTGCCTGGNNNNNNNNNNNNNNNNNNNNNNGAGG 1873

Qy       2042 TGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATT 2101
Db       1874 TGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATGT 1933

Qy       2102 TCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGA 2161
Db       1934 TCAAGGACAGTTACCACAACCTGCGCCTCTCCCTCCATGACCTCCCCCATGCCCATTGGA 1993

Qy       2162 GAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACC 2221
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Db       1994 GGAGCAAGCTGCTGGCCAAATACCAGGAGATCCCCTTCTGTCACATTTGGAGTGGCAGCC 2053

Qy       2222 GGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGT 2281

Db       2054 AGAAGGCCCTCCACTGCACTTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTCA 2113

Qy       2282 CCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACAT 2341

Db       2114 CCTGCAAGATCTGCGTGCGGCAAGTGGAAGGGGAGGGCCAGATATTCCAGCTGCATACCA 2173

Qy       2342 CAATCCTAGAGAGTGAACGAGAAACCAT---CACTTTCTTCGCACAAGAGGACAGCACTT 2398

Db       2174 CTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCCCCTGGCAGCACTG 2233

Qy       2399 TCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTT 2458

Db       2234 TCACCACCCAGCTGGGACCTTATGCCTTCAAGATCCCACTGTCCATCCGCCAGAAGATAT 2293

Qy       2459 GTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAA 2518

Db       2294 GCAACAGCCTAGATGCCCCCAACTCACGGGGCAATGACTGGCGGATGTTAGCACAGAAGC 2353

Qy       2519 ACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTT 2578

Db       2354 TCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATCC 2413

Qy       2579 TGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCC 2638

Db       2414 TGGACCTCTGGGAAGCTCTGCAGCAGGACGATGGGGACCTCAACAGCCTGGCGAGTGCCT 2473

Qy       2639 TTGAAGAGATTGGGAGGA 2656

Db       2474 TGGAGGAGATGGGCAAGA 2491


RESULT 15
BU447189
LOCUS       BU447189                896 bp    mRNA    linear   EST 29-NOV-2002
DEFINITION  603214135F1 CSEQRBN13 Gallus gallus cDNA clone ChEST198e9 5', mRNA
            sequence.
ACCESSION   BU447189
VERSION     BU447189.1  GI:25936500
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
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                     /strain="Layer"
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                     /note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN

  Query Match          14.1%;  Score 386.2;  DB 5;  Length 896;
  Best Local Similarity   82.0%;  Pred. No. 2.8e-101;
  Matches  445;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy       2194 CCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAG 2253

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Qy       2254 CGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGC 2313

Db         62 CGTTACACCCCTGCAACCACACAGCTGTCCTGCAAGATCTGCGTCCGGCAAGTCAAGGGG 121

Qy       2314 CATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACT 2373

Db        122 CACGAGCAGATCCTACAGATCCAGACATCCATCCTCGAGAATGAAAGAGAAACCATTGCT 181

Qy       2374 TTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATT 2433

Db        182 TTCTTTGCACACGATGACAGCAACTTCCCTGCACAGATGGGTGCAAAAGCATTCAAAATC 241

Qy       2434 CCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAG 2493

Db        242 CCATATTCCATCAGACAAAGAATCTGCGCGACGTTCGACACACCCAATGCCAAAGGCAAA 301

Qy       2494 GACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACA 2553

Db        302 GACTGGCAGATGCTAGCACAGAAAAACAGCATCAGCAGGAATCTCTCCTATTTTGCCACA 361

Qy       2554 CAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGT 2613

Db        362 CAAAGCAGTCCATCTGCTGTCATTCTGGACCTCTGGGAAGCCCGACACCAACACGATGGA 421

Qy       2614 GATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCA 2673

Db        422 GACCTCGACTCCCTCGCCTGTGCCCTGGAGGAGATAGGAAGGACACACTCTAAAATCTCA 481

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Db        542 TAG 544


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Job time : 8603 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 23:03:03 ; Search time 1371 Seconds
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Perfect score: 2736
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2736	100.0	3411	13	ADR44610	Adr44610 Novel hum
3	2660	97.2	2703	13	ADR44588	Adr44588 Novel hum
4	2642	96.6	2694	13	ADR44590	Adr44590 Novel hum
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9	2287	83.6	2979	10	ABX17909	Abx17909 cDNA enco
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15	1967	71.9	2010	13	ADR44604	Adr44604 Novel hum
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ALIGNMENTS

RESULT 1
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ID ADR44586 standard; cDNA; 2736 BP.
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AC ADR44586;
XX
DT 04-NOV-2004 (first entry)
XX
DE Novel human protein (NHP) encoding cDNA #5.
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KW Novel human protein; NHP; drug screening; clinical trial monitoring;
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
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FT variation replace(1276,T)
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XX
PD 17-AUG-2004.
XX
PF 02-OCT-2001; 2001US-00969532.
XX
PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Scoville J;
XX

DR WPI; 2004-591302/57.
DR P-PSDB; ADR44587.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Claim 1; SEQ ID NO 9; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
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SQ Sequence 2736 BP; 713 A; 715 C; 695 G; 613 T; 0 U; 0 Other;

Query Match 100.0%; Score 2736; DB 13; Length 2736;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DT 04-NOV-2004 (first entry)
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KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
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OS Homo sapiens.
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PD 17-AUG-2004.
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PF 02-OCT-2001; 2001US-00969532.
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PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Scoville J;
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DR WPI; 2004-591302/57.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Disclosure; SEQ ID NO 33; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
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Query Match 100.0%; Score 2736; DB 13; Length 3411;
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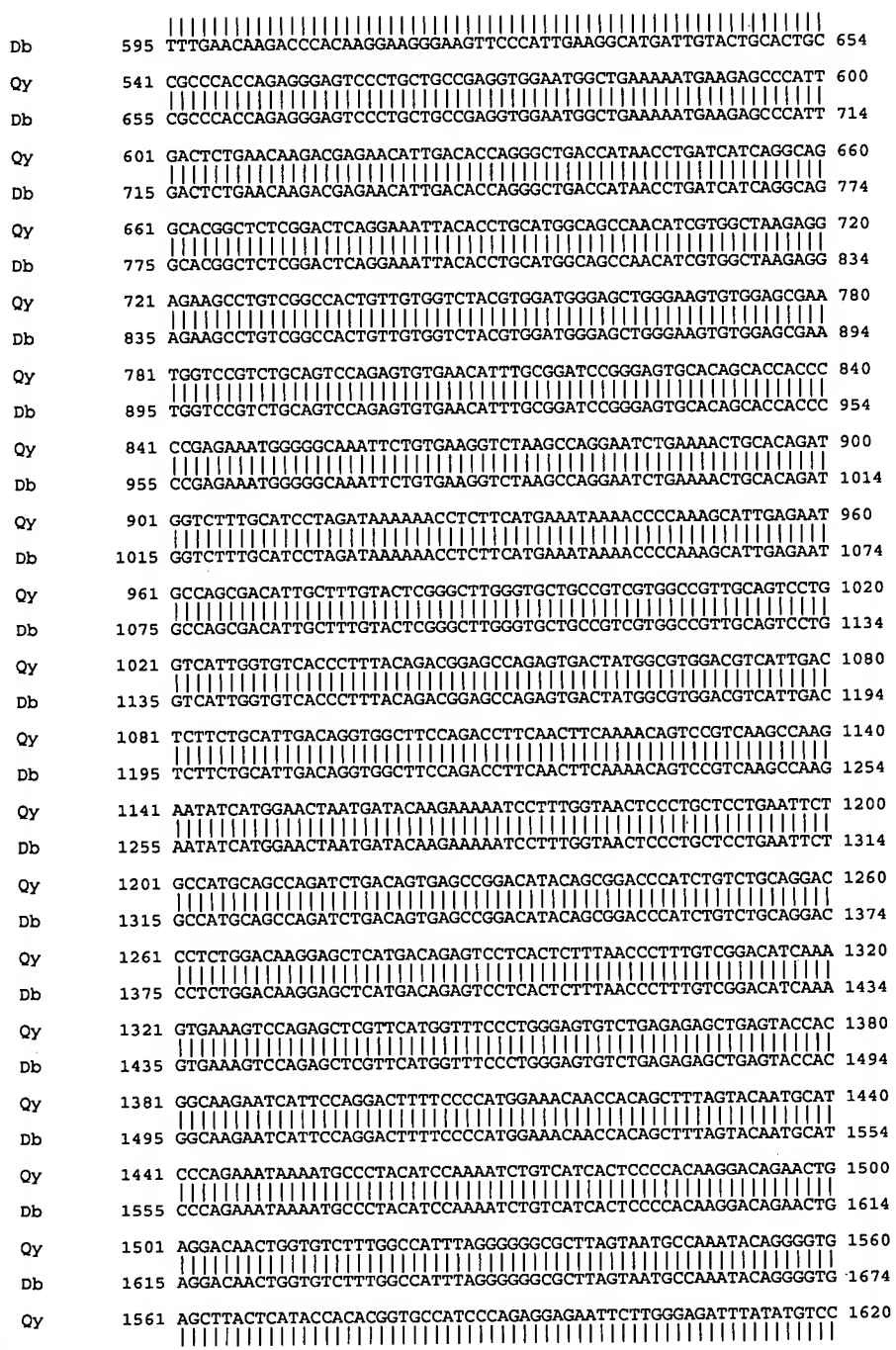
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Db 955 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 1014
Qy 901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
Db 1015 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 1074
Qy 961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
Db 1075 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1134
Qy 1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
Db 1135 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1194
Qy 1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
Db 1195 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1254
Qy 1141 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1200
Db 1255 AATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCCTGCTCCTGAATTCT 1314
Qy 1201 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1260
Db 1315 GCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCATCTGTCTGCAGGAC 1374
Qy 1261 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1320
Db 1375 CCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTTTGTCGGACATCAAA 1434
Qy 1321 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1380
Db 1435 GTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGAGAGCTGAGTACCAC 1494
Qy 1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
Db 1495 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1554
Qy 1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
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Qy 1501 AGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGCCAAATACAGGGGTG 1560
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Qy 1621 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1680
Db 1735 ATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGCTCCTGAGTCCTGAA 1794
Qy 1681 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACCATCCCGCAC 1740
Db 1795 GTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCCTTTGCATTGACCATCCCGCAC 1854
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Qy 1801 AAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTTACTGCCTTTTGGAC 1860
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Db 1975 CCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGCTCACTGGAGAGCCA 2034
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Db 2035 ATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCTGCATGTCCTGTAAC 2094
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Qy 2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
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Qy 2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
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Qy 2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
Db 2455 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2514
Qy 2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
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Qy 2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
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Qy 2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
Db 2635 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2694
Qy 2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
Db 2695 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2754
Qy 2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
Db 2755 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2814

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Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
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Db       2815 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2850
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RESULT 3
ADR44588
ID ADR44588 standard; cDNA; 2703 BP.
XX
AC ADR44588;
XX
DT 04-NOV-2004 (first entry)
XX
DE Novel human protein (NHP) encoding cDNA #6.
XX
KW Novel human protein; NHP; drug screening; clinical trial monitoring;
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
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OS Homo sapiens.
XX
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FT variation replace(776,C)
FT /*tag= b
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FT /*tag= c
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FT variation replace(1243,T)
FT /*tag= d
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PN US6777232-B1.
XX
PD 17-AUG-2004.
XX
PF 02-OCT-2001; 2001US-00969532.
XX
PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Scoville J;
XX
DR WPI; 2004-591302/57.
DR P-PSDB; ADR44589.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Disclosure; SEQ ID NO 11; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
XX
SQ Sequence 2703 BP; 695 A; 707 C; 694 G; 607 T; 0 U; 0 Other;

Query Match 97.2%; Score 2660; DB 13; Length 2703;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2703; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

Qy         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGGGGCTGTGCTTCTGGGCGGCAGGGACCGCGGCTGCCCGAGGAACTGACAATGGCGAA 120

Qy        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180
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Db        121 GCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCCTCATTTCATAGAGGAGCCA 180

Qy        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240
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Db        181 GATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAGGTGCAAAGCGAGGCCAGCC 240

Qy        241 ATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCAGAACGAGCACGTCTCTGAA 300
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Qy        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360
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Db        301 GAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGTGTTCATCAATGTTACTAGG 360

Qy        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420
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Db        361 CAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTGCCAGTGTGTGGCGTGGAGC 420

Qy        421 CACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCATAGCCTATTTACGGAAAAAC 480
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Qy        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540
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Db        481 TTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGGCATGATTGTACTGCACTGC 540

Qy        541 CGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAAAATGAAGAGCCCATT 600
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Db        601 GACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCATAACCTGATCATCAGGCAG 660

Qy        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720
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Db        661 GCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGCCAACATCGTGGCTAAGAGG 720

Qy        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780
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Db        721 AGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGGATGGGAGCTGGGAAGTGTGGAGCGAA 780

Qy        781 TGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGCACCACCC 840
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Qy        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900
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Db        841 CCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTGCACAGAT 900

Qy        901 GGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGCATTGAGAAT 960
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Db        901 GGTCTTTGCATCCTAG----------------------------------GCATTGAGAAT 927

Qy        961 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 1020
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Db        928 GCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGGCCGTTGCAGTCCTG 987

Qy       1021 GTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCGTGGACGTCATTGAC 1080
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Qy       1081 TCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAGTCCGTCAAGCCAAG 1140
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Qy       1381 GGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCTTTAGTACAATGCAT 1440
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Qy       1441 CCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCACAAGGACAGAACTG 1500
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Qy       1561 AGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGGAGATTTATATGTCC 1620
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Qy       1741 TGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGAGGACACAGCAGGGC 1800
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Db       2608 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2667

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Db       2668 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2703
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RESULT 4
ADR44590
ID ADR44590 standard; cDNA; 2694 BP.
XX
AC ADR44590;
XX
DT 04-NOV-2004 (first entry)
XX
DE Novel human protein (NHP) encoding cDNA #7.
XX
KW Novel human protein; NHP; drug screening; clinical trial monitoring;
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
XX
OS Homo sapiens.
XX

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PN US6777232-B1.
XX
PD 17-AUG-2004.
XX

PF 02-OCT-2001; 2001US-00969532.
XX
PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Scoville J;
XX
DR WPI; 2004-591302/57.
DR P-PSDB; ADR44591.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Disclosure; SEQ ID NO 13; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
XX
SQ Sequence 2694 BP; 694 A; 708 C; 689 G; 603 T; 0 U; 0 Other;

Query Match 96.6%; Score 2642; DB 13; Length 2694;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

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Db          1 ATGGGGAGAGCGGCGGCCACCGCAGGCGGCGGCGGAGGGGCGCGCCGCTGGCTCCCGTGG 60

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RESULT 5
ADR44592
ID ADR44592 standard; cDNA; 2661 BP.
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AC ADR44592;
XX
DT 04-NOV-2004 (first entry)
XX
DE Novel human protein (NHP) encoding cDNA #8.
XX
KW Novel human protein; NHP; drug screening; clinical trial monitoring;
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN US6777232-B1.
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PD 17-AUG-2004.
XX
PF 02-OCT-2001; 2001US-00969532.
XX
PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Scoville J;
XX
DR WPI; 2004-591302/57.
DR P-PSDB; ADR44593.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Disclosure; SEQ ID NO 15; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
XX
SQ Sequence 2661 BP; 676 A; 700 C; 688 G; 597 T; 0 U; 0 Other;

Query Match 93.8%; Score 2566; DB 13; Length 2661;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2661; Conservative 0; Mismatches 0; Indels 75; Gaps 2;

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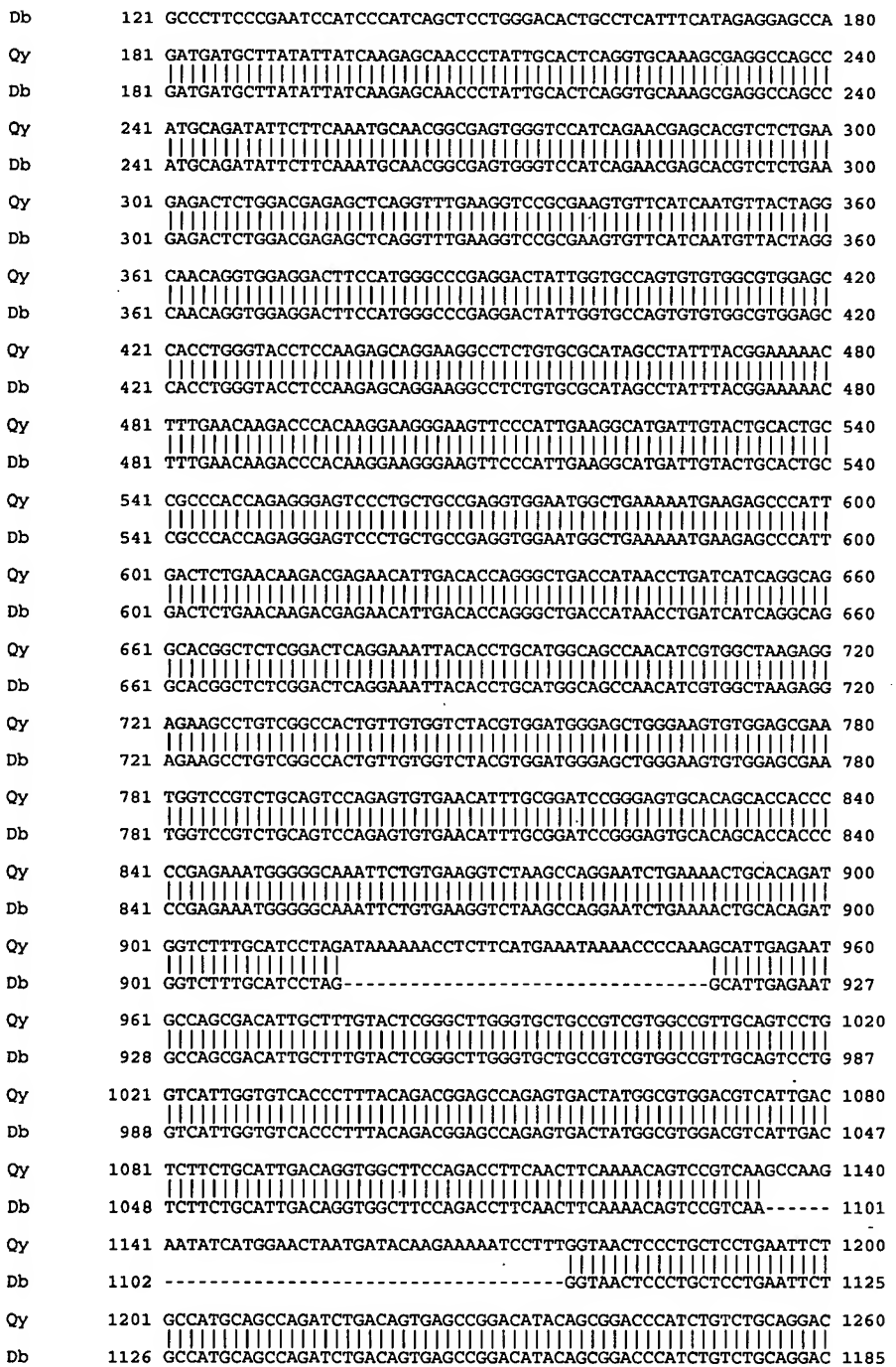
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Qy 1981 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 2040
Db 1906 TCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATTTCAGGAA 1965
Qy 2041 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2100
Db 1966 GTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCAT 2025
Qy 2101 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2160
Db 2026 TTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGG 2085
Qy 2161 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2220
Db 2086 AGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAAC 2145
Qy 2221 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2280
Db 2146 CGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTG 2205
Qy 2281 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2340
Db 2206 TCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACA 2265

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Qy       2341 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 TCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTC 2325

Qy       2401 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 CCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGT 2385

Qy       2461 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 GCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAAC 2445

Qy       2521 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 AGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTG 2505

Qy       2581 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTT 2565

Qy       2641 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCTTGATGAA 2625

Qy       2701 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
             ||||||||||||||||||||||||||||||||||||
Db       2626 GCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2661
```

RESULT 6
ABK88064
ID ABK88064 standard; cDNA; 7002 BP.
XX
AC ABK88064;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA encoding novel human neuroprotective protein.
XX
KW Unc gene family; neuron disorder; neuroprotective; gene therapy; gene;
KW ss; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56. .2902
FT /*tag= a
FT /product= "Novel human neuroprotective protein"
XX
PN JP2002153290-A.
XX
PD 28-MAY-2002.
XX
PF 19-DEC-2000; 2000JP-00385090.
XX
PR 07-SEP-2000; 2000JP-00271068.
XX
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX
DR WPI; 2002-552746/59.
DR P-PSDB; AAU98517.
XX
PT New unc5H4 gene and a protein encoded by it used for the treatment of
PT diseases related to neuron.
XX
PS Claim 2; Page 10-18; 22pp; Japanese.
XX
CC The invention describes a gene, or its variant, having a biological
CC activity equivalent to a protein encoded by unc gene family of a
CC mammalian. The gene is used for treating and preventing neuron disorders
CC and in gene therapy. This sequence encodes the neuroprotective protein
CC showing an activity equivalent to members of the unc gene family
XX

SQ Sequence 7002 BP; 1989 A; 1491 C; 1499 G; 2023 T; 0 U; 0 Other;

Query Match 86.4%; Score 2365.2; DB 6; Length 7002;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 2597; Conservative 0; Mismatches 3; Indels 210; Gaps 2;

```
Qy         95 CTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 154
              || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 CTTCACCAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 194

Qy        155 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 254

Qy        215 CACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGG 274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 CACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGG 314

Qy        275 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 374

Qy        335 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 434

Qy        395 ATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTG 454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTG 494

Qy        455 TGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCA 514
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 TGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCA 554

Qy        515 TTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGG 574
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 TTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGG 614

Qy        575 AATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGG 634
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 AATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGG 674

Qy        635 CTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCA 694
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 CTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCA 734

Qy        695 TGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---- 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 TGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGA 794

Qy        751 ------------------------------------------------------------ 750

Db        795 ATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGAT 854

Qy        751 ------------------------------------------------------------ 750

Db        855 GGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTG 914

Qy        751 ----------------------------------------GTGGATGGGAGCTGGG 766
                                                     ||||||||||||||||
Db        915 AGGGAATGTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGG 974

Qy        767 AAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGT 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 AAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGT 1034

Qy        827 GCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTG 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 GCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTG 1094

Qy        887 AAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCC 946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 AAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCC 1154
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Qy       947 AAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGG 1006
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1155 AAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGG 1214

Qy      1007 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1066
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1215 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1274

Qy      1067 TGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAG 1126
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1275 TGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAG 1334

Qy      1127 TCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCC 1186
            ||||||||                                            ||||||||||
Db      1335 TCCGTCAA----------------------------------------GGTAACTCCC 1352

Qy      1187 TGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCA 1246
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1353 TGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCA 1412

Qy      1247 TCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTT 1306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1413 TCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTT 1472

Qy      1307 TGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1473 TGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1532

Qy      1367 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1426
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1533 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1592

Qy      1427 TTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCA 1486
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1593 TTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCA 1652

Qy      1487 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGC 1546
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1653 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGC 1712

Qy      1547 CAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGG 1606
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1713 CAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGG 1772

Qy      1607 AGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC 1666
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1773 AGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC 1832

Qy      1667 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCAT 1726
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1833 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCAT 1892

Qy      1727 TGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGA 1786
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1893 TGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGA 1952

Qy      1787 GGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 1846
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1953 GGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 2012

Qy      1847 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGC 1906
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2013 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGC 2072

Qy      1907 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 1966
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2073 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 2132

Qy      1967 GCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTT 2026
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2133 GCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTT 2192

Qy      2027 GTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAAC 2086
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2193 GTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAAC 2252

Qy      2087 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2146
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2253 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2312

Qy      2147 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCG 2206
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2313 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCG 2372

Qy      2207 TGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCA 2266
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2373 TGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCA 2432

Qy      2267 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2433 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2492

Qy      2327 TCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAG 2386
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2493 TCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAG 2552

Qy      2387 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCA 2446
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2553 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCA 2612

Qy      2447 GACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2506
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2613 GACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2672

Qy      2507 TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCAT 2566
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2673 TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCAT 2732

Qy      2567 CTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCC 2626
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2733 CTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCC 2792

Qy      2627 TGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAAT 2686
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2793 TGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAAT 2852

Qy      2687 CCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2853 CCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2902
```

RESULT 7
ADP56230
ID ADP56230 standard; cDNA; 7002 BP.
XX
AC ADP56230;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PRO cDNA sequence SEQ ID NO:2206.
XX
KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004039956-A2.
XX
PD 13-MAY-2004.
XX

PF 28-OCT-2003; 2003WO-US034381.
XX
PR 29-OCT-2002; 2002US-0422472P.
XX
PA (GETH) GENENTECH INC.
XX
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-376182/35.
DR P-PSDB; ADP56231.
XX
PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX
PS Claim 2; SEQ ID NO 2206; 3009pp; English.
XX
CC The present invention describes an isolated PRO nucleic acid (I). Also
CC described: (1) a vector comprising (I); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC ; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO nucleotide sequence from the present invention.
XX
SQ Sequence 7002 BP; 1989 A; 1491 C; 1499 G; 2023 T; 0 U; 0 Other;

Query Match 86.4%; Score 2365.2; DB 13; Length 7002;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 2597; Conservative 0; Mismatches 3; Indels 210; Gaps 2;

```
Qy    95 CTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 154
Db   135 CTTCACCAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGA 194

Qy   155 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 214
Db   195 CACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTG 254

Qy   215 CACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGG 274
Db   255 CACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGG 314

Qy   275 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 334
Db   315 TCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCC 374

Qy   335 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 394
Db   375 GCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACT 434

Qy   395 ATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTG 454
Db   435 ATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTG 494

Qy   455 TGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCA 514
Db   495 TGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCA 554

Qy   515 TTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGG 574
Db   555 TTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGG 614

Qy   575 AATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGG 634
Db   615 AATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGG 674

Qy   635 CTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCA 694
Db   675 CTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCA 734

Qy   695 TGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---- 750
Db   735 TGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGA 794

Qy   751 ---------- 750
Db   795 ATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGAT 854

Qy   751 ---------- 750
Db   855 GGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTG 914

Qy   751 ----------GTGGATGGGAGCTGGG 766
Db   915 AGGGAATGTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGG 974

Qy   767 AAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGT 826
Db   975 AAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGT 1034

Qy   827 GCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTG 886
Db  1035 GCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTG 1094

Qy   887 AAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCC 946
Db  1095 AAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCC 1154

Qy   947 AAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGG 1006
Db  1155 AAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCGTCGTGG 1214

Qy  1007 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1066
Db  1215 CCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACTATGGCG 1274

Qy  1067 TGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAG 1126
Db  1275 TGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCAAAACAG 1334

Qy  1127 TCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTAACTCCC 1186
Db  1335 TCCGTCAA----------GGTAACTCCC 1352

Qy  1187 TGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCA 1246
Db  1353 TGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCGGACCCA 1412

Qy  1247 TCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTT 1306
Db  1413 TCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTAACCCTT 1472

Qy  1307 TGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1366
```

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Db      1473 TGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGTCTGAGA 1532

Qy      1367 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1426

Db      1533 GAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACCACAGCT 1592

Qy      1427 TTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCA 1486

Db      1593 TTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCACTCCCCA 1652

Qy      1487 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGC 1546

Db      1653 CAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAGTAATGC 1712

Qy      1547 CAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGG 1606

Db      1713 CAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATTCTTGGG 1772

Qy      1607 AGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC 1666

Db      1773 AGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTGAGGTGC 1832

Qy      1667 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCAT 1726

Db      1833 TCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCTTTGCAT 1892

Qy      1727 TGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGA 1786

Db      1893 TGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAAAGAAGA 1952

Qy      1787 GGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 1846

Db      1953 GGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACATCCTGTT 2012

Qy      1847 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGC 1906

Db      2013 ACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCTATGCGC 2072

Qy      1907 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 1966

Db      2073 TCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTTTTGGCT 2132

Qy      1967 GCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTT 2026

Db      2133 GCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTT 2192

Qy      2027 GTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAAC 2086

Db      2193 GTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAAC 2252

Qy      2087 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2146

Db      2253 CAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTC 2312

Qy      2147 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCG 2206

Db      2313 CCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCG 2372

Qy      2207 TGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCA 2266

Db      2373 TGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCA 2432

Qy      2267 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2326

Db      2433 CTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCC 2492

Qy      2327 TCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAG 2386

Db      2493 TCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAG 2552

Qy      2387 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCA 2446

Db      2553 AGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCA 2612

Qy      2447 GACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2506

Db      2613 GACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGT 2672

Qy      2507 TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCAT 2566

Db      2673 TAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCAT 2732

Qy      2567 CTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCC 2626

Db      2733 CTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCC 2792

Qy      2627 TGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAAT 2686

Db      2793 TGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAAT 2852

Qy      2687 CCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736

Db      2853 CCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2902
```

RESULT 8
ADQ24624
ID ADQ24624 standard; DNA; 8899 BP.
XX
AC ADQ24624;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7444.
XX
KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 7444; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX

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SQ   Sequence 8899 BP; 2581 A; 1815 C; 1817 G; 2575 T; 0 U; 111 Other;

  Query Match            84.8%;  Score 2320.8;  DB 12;  Length 8899;
  Best Local Similarity  90.6%;  Pred. No. 0;
  Matches 2552;  Conservative    0;  Mismatches   54;  Indels  210;  Gaps    2;

Qy         89 CCGCGGCTGCCCGAGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTC 148
              ||                                                  ||||||||||
Db        129 CCCANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCCGAATCCATCCCATCAGCTC 188

Qy        149 CTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACC 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTGGGACACTGCCTCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACC 248

Qy        209 CTATTGCACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCG 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CTATTGCACTCAGGTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCG 308

Qy        269 AGTGGGTCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGA 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 AGTGGGTCCATCAGAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGA 368

Qy        329 AGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGGTCCGCGAAGTGTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCG 428

Qy        389 AGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGG 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 AGGACTATTGGTGCCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGG 488

Qy        449 CCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAG 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CCTCTGTGCGCATAGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAG 548

Qy        509 TTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCG 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 TTCCCATTGAAGGCATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCG 608

Qy        569 AGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACA 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 AGGTGGAATGGCTGAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACA 668

Qy        629 CCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACA 688
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CCAGGGCTGACCATAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACA 728

Qy        689 CCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCT 748
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 CCTGCATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCT 788

Qy        749 AC------------------------------------------------------------ 750
              ||
Db        789 ACGTGAATGGAGGCTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTA 848

Qy        751 ------------------------------------------------------------ 750

Db        849 GAGGATGGCAGAAACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCT 908

Qy        751 ----------------------------------------------------GTGGATGGGA 760
                                                                   ||||||||||
Db        909 TTTGTGAGGGAATGTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGA 968

Qy        761 GCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCC 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 GCTGGGAAGTGTGGAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCC 1028

Qy        821 GGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGG 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 GGGAGTGCACAGCACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGG 1088

Qy        881 AATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAA 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 AATCTGAAAACTGCACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAA 1148

Qy        941 AACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCG 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 AACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGCTGCCG 1208

Qy       1001 TCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACT 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 TCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAGTGACT 1268

Qy       1061 ATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCA 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 ATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAACTTCA 1328

Qy       1121 AAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTTTGGTA 1180
              |||||||||||||||                                        ||||
Db       1329 AAACAGTCCGTCAA----------------------------------------GGTA 1346

Qy       1181 ACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCG 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 ACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATACAGCG 1406

Qy       1241 GACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTA 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1407 GACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACTCTTTA 1466

Qy       1301 ACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGT 1360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 ACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGGAGTGT 1526

Qy       1361 CTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACC 1420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1527 CTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAACAACC 1586

Qy       1421 ACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1587 ACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTCATCAC 1646

Qy       1481 TCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1647 TCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCGCTTAG 1706

Qy       1541 TAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATT 1600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1707 TAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGAGAATT 1766

Qy       1601 CTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTG 1660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1767 CTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGGCTCTG 1826

Qy       1661 AGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCT 1720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1827 AGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCACTCCCT 1886

Qy       1721 TTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAA 1780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1887 TTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTTAA 1946

Qy       1781 AGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACAT 1840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1947 AGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATCTACAT 2006

Qy       1841 CCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCT 1900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2007 CCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGGGACCT 2066

Qy       1901 ATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTT 1960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2067 ATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGCGGTTT 2126

Qy       1961 TTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATA 2020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2127 TTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTANNNNNNNNNNNNNN 2186
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Qy       2021 CCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGG 2080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2187 NNNCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGG 2246

Qy       2081 AAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTG 2140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2247 AAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTG 2306

Qy       2141 ATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCT 2200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2307 ATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCT 2366

Qy       2201 CCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATA 2260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2367 CCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATA 2426

Qy       2261 CGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAAC 2320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2427 CGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAAC 2486

Qy       2321 AGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCG 2380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2487 AGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCG 2546

Qy       2381 CACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACT 2440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2547 CACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACT 2606

Qy       2441 CCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGC 2500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2607 CCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGC 2666

Qy       2501 AGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTA 2560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2667 AGATGTTAGCACAGAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTA 2726

Qy       2561 GCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTG 2620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2727 GCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTG 2786

Qy       2621 ACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTT 2680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2787 ACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTT 2846

Qy       2681 CAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2847 CAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTCTAG 2902
```

RESULT 9
ABX17909
ID ABX17909 standard; cDNA; 2979 BP.
XX
AC ABX17909;
XX
DT 06-FEB-2003 (first entry)
XX
DE cDNA encoding human G-protein coupled receptor GCREC-63.
XX
KW Human; G-protein coupled receptor; GPCR; GCREC; INTSIG; cancer;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW diabetes; Grave's disease; leukaemia; cervical cancer; breast cancer;
KW immunological disorder; scleroderma; systemic lupus erythematosus;
KW allergy; gastrointestinal disorder; Crohn's disease; renal disorder;
KW Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic;
KW protozoal; helminthic; cardiovascular disorder; atherosclerosis;
KW hepatic disease; cirrhosis; transgenic; neuroprotective; relaxant;
KW antithyroid; cytostatic; dermatological; immunosuppressive; uropathic;
KW thyromimetic; antiinflammatory; cerebroprotective; gastrointestinal;
KW hepatotropic; nephrotropic; anticonvulsant; antirheumatic; cardiant;
KW nootropic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200279448-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009923.
XX
PR 30-MAR-2001; 2001US-0280683P.
PR 13-APR-2001; 2001US-0283714P.
PR 20-APR-2001; 2001US-0285336P.
PR 27-APR-2001; 2001US-0287266P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Thornton M, Yao MG, Richardson TW, Swarnakar A, Kallick DA;
PI Ison CH, Walia NK, Gandhi AR, Lee EA, Elliott VS, Hafalia AJA;
PI Au-Young J, Griffin JA, Baughn MR, Khan FA, Becha S, Lu Y;
PI Arvizu CP, Borowsky ML, Lal PG, Ramkumar J, Emerling BM, Walsh RT;
PI Yue H, Burford N, Graul RC;
XX
DR WPI; 2003-058430/05.
DR P-PSDB; ABU11210.
XX
PT New GCREC polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with an abnormal expression or activity of GCREC,
PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer and
PT infection.
XX
PS Claim 5; Page 307-308; 313pp; English.
XX
CC The present invention relates to the isolation of human G-protein coupled
CC receptors (GPCRs, designated GCREC), and the polynucleotide sequences
CC encoding them. The GCREC polypeptides or their fragments, and the
CC polynucleotides sequences encoding them are useful in diagnosing,
CC preventing, and treating disorders associated with an abnormal expression
CC or activity of INTSIG, such as neurodegenerative disorders (e.g.
CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.
CC myotonic dystrophy, catatonia), endocrine disorders (e.g. diabetes,
CC Grave's disease), cancers (e.g. leukaemia, cervical or breast cancers),
CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,
CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal
CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral,
CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular
CC disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis).
CC GCREC or its fragments may also be used in screening for compounds that
CC specifically bind to and modulate the activity of GCREC. The
CC polynucleotides can be used to create humanised animals or transgenic
CC animals to model human disease. ABX17847-ABX17919 represent cDNA
CC sequences encoding the human GCRECs of the invention
XX
SQ Sequence 2979 BP; 764 A; 766 C; 740 G; 709 T; 0 U; 0 Other;

Query Match 83.6%; Score 2287; DB 10; Length 2979;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2560; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

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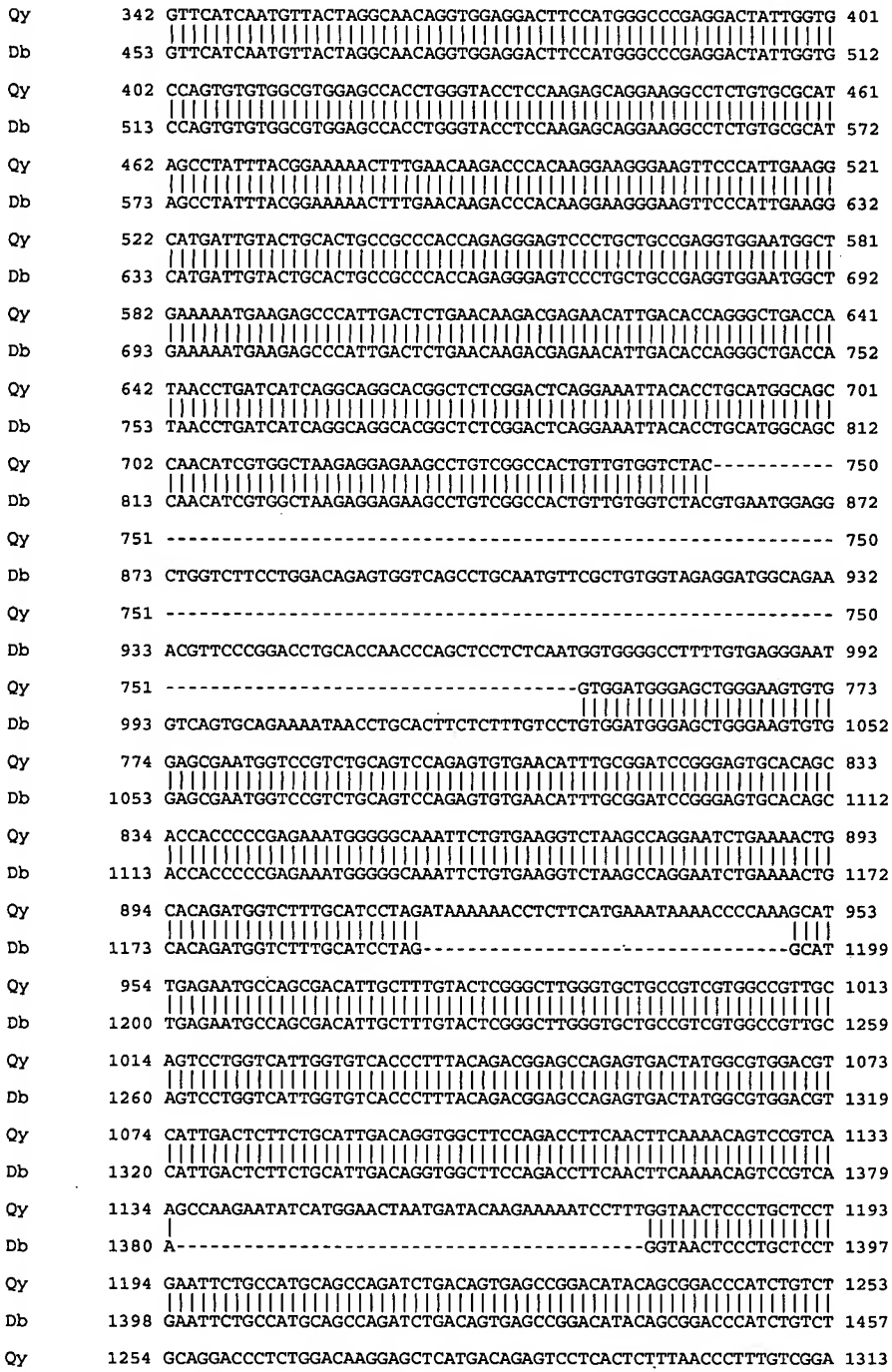
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Db 573 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 632
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RESULT 10
ADC77423
ID   ADC77423 standard; DNA; 2868 BP.
XX
AC   ADC77423;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human transmembrane protein INSP017 full length cDNA sequence.
XX
KW   INSP017; transmembrane protein; netrin receptor family; netrin; axion;
KW   cell migration; axon path-finding; central nervous system;
KW   inflammatory disease; oncology; cardiovascular disease; cytostatic;
KW   antiinflammatory; immunosuppressive; cardiant; anti-HIV; neuroprotective;
KW   nootropic; antiparkinsonian; antidepressant; neuroleptic; osteopathic;
KW   antiarteriosclerotic; nephrotropic; immunomodulator; antidiabetic;
KW   antiinfertility; gene therapy; cell proliferative disorder;
KW   myeloproliferative disorder; autoimmune disorder; inflammatory disorder;
KW   cardiovascular disorder; neurological disorder; psychiatric disorder;
KW   developmental disorder; bone disease; atherosclerosis;
KW   glomerulonephritis; AIDS; HIV infection; metabolic disorder;
KW   pregnancy disorder; birth complication; human; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /partial
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PN   WO2003055915-A2.
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PD   10-JUL-2003.
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PF   20-DEC-2002; 2002WO-GB005856.
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PR   21-DEC-2001; 2001GB-00030721.
XX
PA   (ARES-) ARES TRADING SA.
XX
PI   Fitzgerald SN,  Fagan RJ,  Phelps CB,  Power C,  Yorke M;
XX
DR   WPI; 2003-559270/52.
DR   P-PSDB; ADC77424.
XX
PT   New polypeptide, useful for the manufacture of a medicament for treating
PT   disease, e.g., cell proliferative, autoimmune, inflammatory,
PT   cardiovascular or neurological disorders.
XX
PS   Claim 9; SEQ ID NO 33; 96pp; English.
XX
CC   This invention relates to a novel human protein (INSP017), a
CC   transmembrane protein of the netrin receptor family, and to the use of
CC   this protein and the DNA sequence which encodes it for diagnosis,
CC   prevention and treatment of disease. Netrins are a family of secreted
CC   proteins which are involved in both repelling and attracting axions and
CC   thus function as guidance molecules for cell migration and axon path-
CC   finding processes in the central nervous system. Transmembrane proteins
CC   such as that of the invention have been shown to play a role in diverse
CC   physiological functions and they may be involved in many diseases,
CC   particularly inflammatory diseases, oncology and cardiovascular disease.
CC   Compounds which modulate the transmembrane protein of the invention may
CC   therefore have cytostatic, antiinflammatory, immunosuppressive, cardiant,
CC   anti-HIV, neuroprotective, nootropic, antiparkinsonian, antidepressant,
CC   neuroleptic, osteopathic, antiarteriosclerotic, nephrotropic,
CC   immunomodulator, antidiabetic or antiinfertility activity. In addition,
CC   the protein and amino acid sequence of the invention may be useful for
CC   gene therapy. The protein, nucleic acid (and compound and pharmaceutical
CC   composition) of the invention may be useful for the manufacture of a
CC   medicament for treating disease, such as cell proliferative disorders,
CC   myeloproliferative disorders, autoimmune/inflammatory disorders,
CC   cardiovascular disorders, neurological disorders, psychiatric disorders,
CC   developmental disorders, bone disease, atherosclerosis,
CC   glomerulonephritis, AIDS, HIV infections, metabolic disorders, pregnancy
CC   disorders and birth complications. The present sequence is the cloned
CC   cDNA sequence which encodes the protein INSP017 of the invention.
XX
SQ   Sequence 2868 BP; 732 A; 748 C; 714 G; 674 T; 0 U; 0 Other;
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Query Match 83.5%; Score 2284; DB 10; Length 2868;
Best Local Similarity 91.3%; Pred. No. 0;
Matches 2557; Conservative 0; Mismatches 0; Indels 243; Gaps 3;

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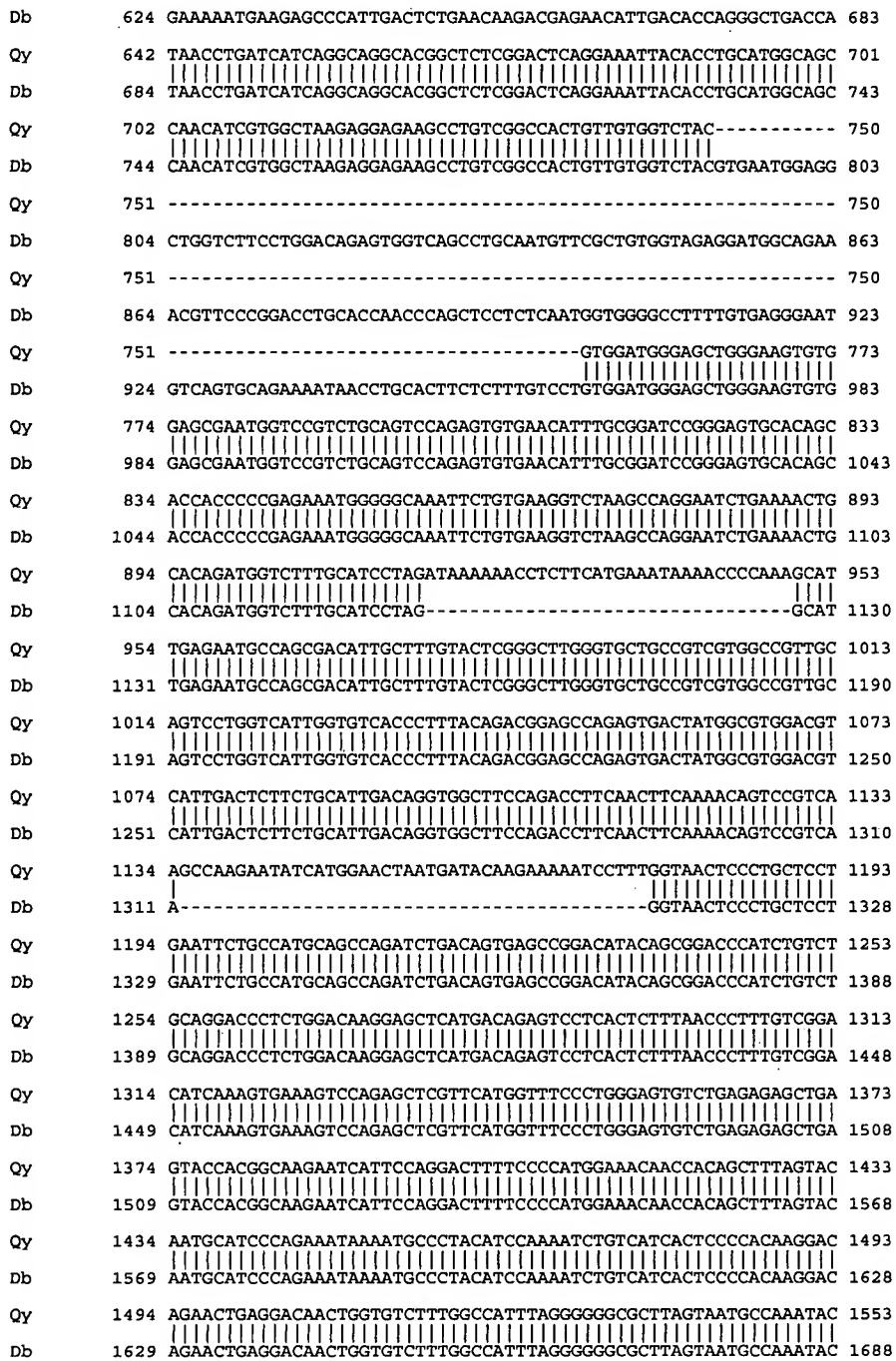
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Qy 1974 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2033
Db 2109 CTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGACAATACCCCTTGTGCATT 2168
Qy 2034 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2093
Db 2169 TCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATT 2228
Qy 2094 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2153
Db 2229 GCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATT 2288
Qy 2154 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2213
Db 2289 CCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTG 2348
Qy 2214 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2273
Db 2349 CAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCAC 2408
Qy 2274 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2333
Db 2409 CCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGT 2468
Qy 2334 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2393
Db 2469 GCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAG 2528
Qy 2394 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2453
Db 2529 CACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCG 2588
Qy 2454 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2513
Db 2589 GATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACA 2648
Qy 2514 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2573
Db 2649 GAAAAACAGCATCAACAGGAATTTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGT 2708
Qy 2574 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2633
Db 2709 CATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTG 2768

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Qy       2634 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2693
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Db       2769 TGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTCAAACATTTCAGAATCCCAGCT 2828

Qy       2694 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2733
             |||||||||||||||||||||||||||||||||||||||
Db       2829 TGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACTC 2868


RESULT 11
ABX70459
ID   ABX70459 standard; DNA; 2898 BP.
XX
AC   ABX70459;
XX
DT   03-MAR-2003  (first entry)
XX
DE   DNA encoding human GPCR related protein NOV23a.
XX
KW   Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200279398-A2.
XX
PD   10-OCT-2002.
XX
PF   08-MAR-2002; 2002WO-US007355.
XX
PR   08-MAR-2001; 2001US-0274194P.
PR   08-MAR-2001; 2001US-0274281P.
PR   08-MAR-2001; 2001US-0274322P.
PR   09-MAR-2001; 2001US-0274849P.
PR   13-MAR-2001; 2001US-0275578P.
PR   13-MAR-2001; 2001US-0275579P.
PR   13-MAR-2001; 2001US-0275601P.
PR   14-MAR-2001; 2001US-0276000P.
PR   16-MAR-2001; 2001US-0276776P.
PR   19-MAR-2001; 2001US-0276994P.
PR   20-MAR-2001; 2001US-0277239P.
PR   20-MAR-2001; 2001US-0277327P.
PR   20-MAR-2001; 2001US-0277338P.
PR   21-MAR-2001; 2001US-0277791P.
PR   22-MAR-2001; 2001US-0277833P.
PR   23-MAR-2001; 2001US-0278152P.
PR   26-MAR-2001; 2001US-0278894P.
PR   27-MAR-2001; 2001US-0278999P.
PR   27-MAR-2001; 2001US-0279036P.
PR   30-MAR-2001; 2001US-0280233P.
PR   02-APR-2001; 2001US-0280802P.
PR   02-MAY-2001; 2001US-0288052P.
PR   02-MAY-2001; 2001US-0288066P.
PR   02-MAY-2001; 2001US-0288228P.
PR   17-MAY-2001; 2001US-0291766P.
PR   07-JUN-2001; 2001US-0296693P.
PR   08-JUN-2001; 2001US-0296856P.
PR   05-JUL-2001; 2001US-0303230P.
PR   05-JUL-2001; 2001US-0303237P.
PR   08-AUG-2001; 2001US-0310913P.
PR   13-AUG-2001; 2001US-0311978P.
PR   14-AUG-2001; 2001US-0312191P.
PR   16-AUG-2001; 2001US-0312916P.
PR   17-AUG-2001; 2001US-0313182P.
PR   20-AUG-2001; 2001US-0313626P.
PR   21-AUG-2001; 2001US-0314018P.
PR   27-AUG-2001; 2001US-0315227P.
PR   10-SEP-2001; 2001US-0318403P.
PR   10-SEP-2001; 2001US-0318510P.
PR   14-SEP-2001; 2001US-0322296P.
PR   14-SEP-2001; 2001US-0322360P.
PR   27-SEP-2001; 2001US-0325378P.
PR   09-NOV-2001; 2001US-0332486P.
PR   09-NOV-2001; 2001US-0345399P.
PR   07-MAR-2002; 2002US-00094886.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
PI   Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
PI   Guo X, Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ;
PI   Pena CEA, Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;
PI   Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;
PI   Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;
XX
DR   WPI; 2003-058423/05.
DR   P-PSDB; ABU52368.
XX
PT   NOVX polypeptides and polynucleotides, useful for treating a syndrome
PT   related to a human disease associated with the NOVX polypeptide e.g.,
PT   cancer.
XX
PS   Claim 23; Page 158-159; 413pp; English.
XX
CC   The present invention relates to the isolation of novel human
CC   polypeptides referred to as NOVX (NOV1-NOV44), variants of these
CC   proteins, and the polynucleotide sequences encoding them. The NOVX
CC   proteins of the invention are G-protein coupled receptor (GPCR) related
CC   proteins. The sequences of the invention are useful in the manufacture of
CC   a medicament for treating a syndrome related to a human disease
CC   associated with the polypeptides e.g. cancer. ABX70402-ABX70499 represent
CC   DNAs encoding the human NOVX proteins of the invention
XX
SQ   Sequence 2898 BP; 750 A; 759 C; 726 G; 663 T; 0 U; 0 Other;

  Query Match            82.6%;  Score 2260;  DB 8;  Length 2898;
  Best Local Similarity  90.7%;  Pred. No. 0;
  Matches 2562;  Conservative    0;  Mismatches   25;  Indels  237;  Gaps    5;

Qy        102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 157

Qy        162 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 217

Qy        222 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 277

Qy        282 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 337

Qy        342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 397

Qy        402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 457

Qy        462 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 517

Qy        522 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 577

Qy        582 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 637

Qy        642 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 701
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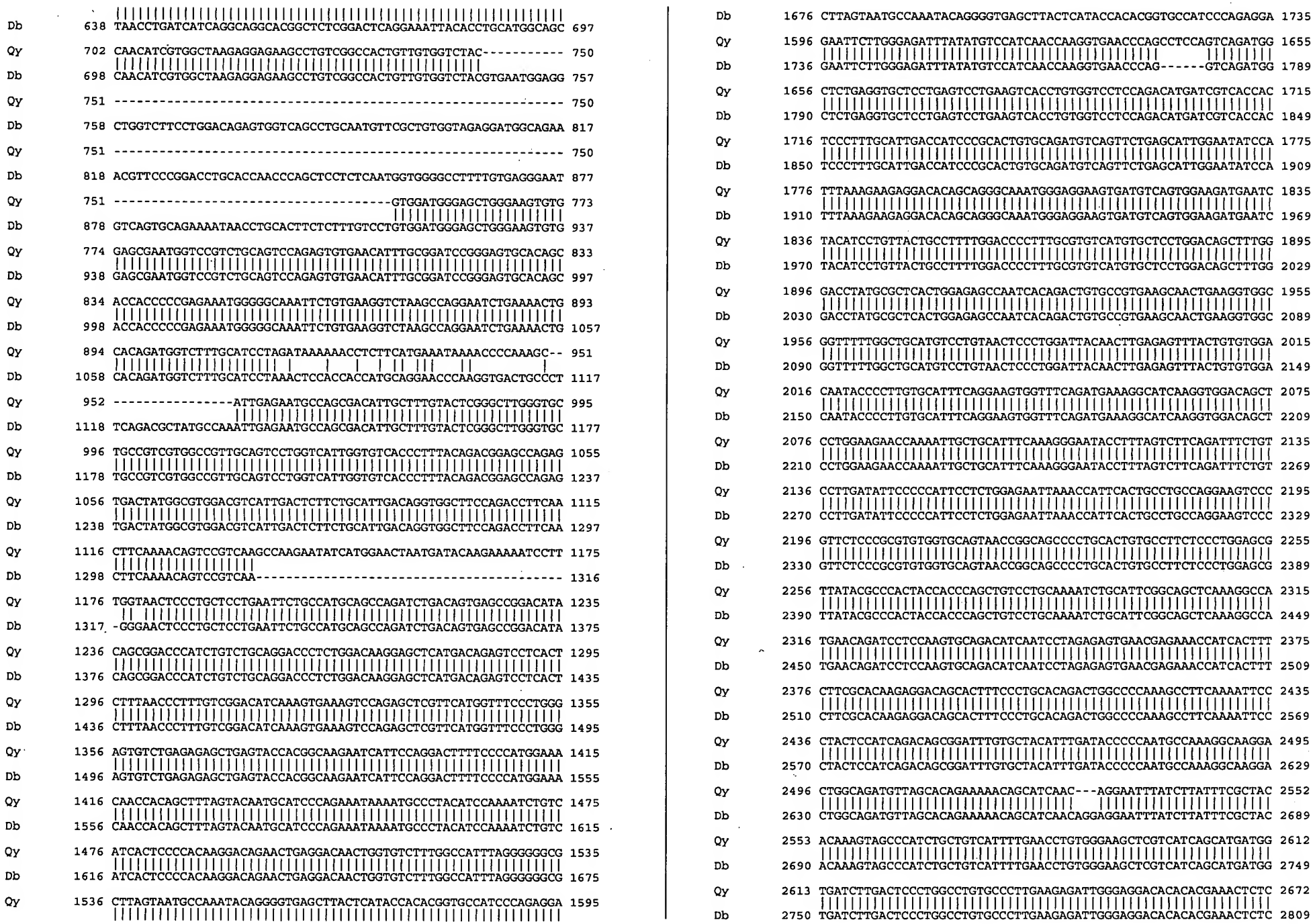
Db 638 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 697
Qy 702 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---------- 750
Db 698 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGAATGGAGG 757
Qy 751 ---------- 750
Db 758 CTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAGAA 817
Qy 751 ---------- 750
Db 818 ACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTGAGGGAAT 877
Qy 751 ----------GTGGATGGGAGCTGGGAAGTGTG 773
Db 878 GTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 937
Qy 774 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 833
Db 938 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 997
Qy 834 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 893
Db 998 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 1057
Qy 894 CACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGC-- 951
Db 1058 CACAGATGGTCTTTGCATCCTAAACTCCACCACCATGCAGGAACCCAAGGTGACTGCCCT 1117
Qy 952 ----------ATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 995
Db 1118 TCAGACGCTATGCCAAATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 1177
Qy 996 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1055
Db 1178 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1237
Qy 1056 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1115
Db 1238 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1297
Qy 1116 CTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTT 1175
Db 1298 CTTCAAAACAGTCCGTCAA---------- 1316
Qy 1176 TGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1235
Db 1317 -GGGAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1375
Qy 1236 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1295
Db 1376 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1435
Qy 1296 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1355
Db 1436 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1495
Qy 1356 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1415
Db 1496 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1555
Qy 1416 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1475
Db 1556 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1615
Qy 1476 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1535
Db 1616 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1675
Qy 1536 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1595
Db 1676 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1735
Qy 1596 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGG 1655
Db 1736 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG------GTCAGATGG 1789
Qy 1656 CTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCAC 1715
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Qy 1716 TCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCA 1775
Db 1850 TCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCA 1909
Qy 1776 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1835
Db 1910 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1969
Qy 1836 TACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGG 1895
Db 1970 TACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGG 2029
Qy 1896 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 1955
Db 2030 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 2089
Qy 1956 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2015
Db 2090 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2149
Qy 2016 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2075
Db 2150 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2209
Qy 2076 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2135
Db 2210 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2269
Qy 2136 CCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCC 2195
Db 2270 CCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCC 2329
Qy 2196 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2255
Db 2330 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2389
Qy 2256 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2315
Db 2390 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2449
Qy 2316 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2375
Db 2450 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2509
Qy 2376 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2435
Db 2510 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2569
Qy 2436 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2495
Db 2570 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2629
Qy 2496 CTGGCAGATGTTAGCACAGAAAAACAGCATCAAC---AGGAATTTATCTTATTTCGCTAC 2552
Db 2630 CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAGGAATTTATCTTATTTCGCTAC 2689
Qy 2553 ACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGG 2612
Db 2690 ACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGG 2749
Qy 2613 TGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTC 2672
Db 2750 TGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTC 2809

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Qy       2673 AAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACT 2732
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Db       2810 AAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACT 2869

Qy       2733 CTAG 2736
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Db       2870 CTAG 2873
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RESULT 12
ADL24070
ID ADL24070 standard; cDNA; 2898 BP.
XX
AC ADL24070;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOVX cDNA #58.
XX
KW Human; NOVX; gene; ss; G protein-coupled receptor; GPCR; cardiomyopathy;
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
KW atrial septal defect; ASD; atrioventricular canal defect;
KW ductus arteriosus; pulmonary stenosis; subaortic stenosis;
KW ventricular septal defect; VSD; tuberous sclerosis; scleroderma; obesity;
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
KW neoplasm; adenocarcinoma; lymphoma; uterine cancer; haemophilia;
KW hypercoagulability; idiopathic thrombocytopenia purpura;
KW immunodeficiency; graft-versus-host disease; AIDS; bronchial asthma;
KW Crohn's disease; multiple sclerosis;
KW Albright's hereditary osteodystrophy; diabetes; infectious diseases;
KW anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; haematopoietic disorder; metabolic disorder.
XX
OS Homo sapiens.
XX
PN US2004002120-A1.
XX
PD 01-JAN-2004.
XX
PF 07-MAR-2002; 2002US-00094886.
XX
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-MAY-2001; 2001US-0288052P.
PR 02-MAY-2001; 2001US-0288066P.
PR 02-MAY-2001; 2001US-0288228P.
PR 17-MAY-2001; 2001US-0291766P.
PR 07-JUN-2001; 2001US-0296693P.
PR 08-JUN-2001; 2001US-0296856P.
PR 05-JUL-2001; 2001US-0303230P.
PR 05-JUL-2001; 2001US-0303237P.
PR 08-AUG-2001; 2001US-0310913P.
PR 13-AUG-2001; 2001US-0311978P.
PR 14-AUG-2001; 2001US-0312191P.
PR 16-AUG-2001; 2001US-0312916P.
PR 17-AUG-2001; 2001US-0313182P.
PR 20-AUG-2001; 2001US-0313626P.
PR 21-AUG-2001; 2001US-0314018P.
PR 27-AUG-2001; 2001US-0315227P.
PR 10-SEP-2001; 2001US-0318403P.
PR 10-SEP-2001; 2001US-0318510P.
PR 14-SEP-2001; 2001US-0322296P.
PR 14-SEP-2001; 2001US-0322360P.
PR 27-SEP-2001; 2001US-0325378P.
PR 09-NOV-2001; 2001US-0332486P.
PR 09-NOV-2001; 2001US-0345399P.
XX
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
XX
PI Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
PI Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
PI Guo X, Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ;
PI Pena CEA, Gangolli EA, Gusev VY, Smithson G, Zerhusen BD, Gerlach V;
PI Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;
PI Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;
XX
DR WPI; 2004-212692/20.
DR P-PSDB; ADL24071.
XX
PT Novel isolated G protein-coupled receptor polypeptides, referred as NOVX,
PT useful for treating scleroderma, obesity, congenital adrenal hyperplasia,
PT prostate cancer, hemophilia, AIDS, bronchial asthma, Crohn's disease.
XX
PS Claim 23; SEQ ID NO 115; 287pp; English.
XX
CC The invention relates to human G protein-coupled receptor-related (GPCR-
CC related) polypeptides (designated NOVX) and the polynucleotides encoding
CC them. The polypeptides and polynucleotides are useful as therapeutics in
CC the manufacture of medicaments for treating syndromes associated with
CC human diseases. The sequences are useful for treating a disorder
CC associated with aberrant NOVX expression or activity such as
CC cardiomyopathy, atherosclerosis, hypertension, congenital heart defects,
CC aortic stenosis, atrial septal defect (ASD), atrioventricular canal

```
CC   defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis,
CC   ventricular septal defect (VSD), tuberous sclerosis, scleroderma,
CC   obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate
CC   cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, haemophilia,
CC   hypercoagulability, idiopathic thrombocytopenia purpura,
CC   immunodeficiencies, graft-versus-host disease, AIDS, bronchial asthma,
CC   Crohn's disease, multiple sclerosis, Albright's hereditary
CC   osteodystrophy, diabetes, infectious diseases, anorexia,
CC   neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC   immune disorders, haematopoietic disorders and metabolic disorders. This
CC   sequence represents human NOVX cDNA of the invention.
XX
SQ   Sequence 2898 BP; 750 A; 760 C; 725 G; 663 T; 0 U; 0 Other;

  Query Match             82.6%;  Score 2260;  DB 12;  Length 2898;
  Best Local Similarity   90.7%;  Pred. No. 0;
  Matches 2562;  Conservative    0;  Mismatches   25;  Indels  237;  Gaps    5;

Qy        102 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 AGGAACTGACAATGGCGAAGCCCTTCCCGAATCCATCCCATCAGCTCCTGGGACACTGCC 157

Qy        162 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 TCATTTCATAGAGGAGCCAGATGATGCTTATATTATCAAGAGCAACCCTATTGCACTCAG 217

Qy        222 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GTGCAAAGCGAGGCCAGCCATGCAGATATTCTTCAAATGCAACGGCGAGTGGGTCCATCA 277

Qy        282 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GAACGAGCACGTCTCTGAAGAGACTCTGGACGAGAGCTCAGGTTTGAAGGTCCGCGAAGT 337

Qy        342 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GTTCATCAATGTTACTAGGCAACAGGTGGAGGACTTCCATGGGCCCGAGGACTATTGGTG 397

Qy        402 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCAGTGTGTGGCGTGGAGCCACCTGGGTACCTCCAAGAGCAGGAAGGCCTCTGTGCGCAT 457

Qy        462 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AGCCTATTTACGGAAAAACTTTGAACAAGACCCACAAGGAAGGGAAGTTCCCATTGAAGG 517

Qy        522 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CATGATTGTACTGCACTGCCGCCCACCAGAGGGAGTCCCTGCTGCCGAGGTGGAATGGCT 577

Qy        582 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 GAAAAATGAAGAGCCCATTGACTCTGAACAAGACGAGAACATTGACACCAGGGCTGACCA 637

Qy        642 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 TAACCTGATCATCAGGCAGGCACGGCTCTCGGACTCAGGAAATTACACCTGCATGGCAGC 697

Qy        702 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTAC---------- 750
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTGAATGGAGG 757

Qy        751 ---------------------------------------------------------- 750

Db        758 CTGGTCTTCCTGGACAGAGTGGTCAGCCTGCAATGTTCGCTGTGGTAGAGGATGGCAGAA 817

Qy        751 ---------------------------------------------------------- 750

Db        818 ACGTTCCCGGACCTGCACCAACCCAGCTCCTCTCAATGGTGGGGCCTTTTGTGAGGGAAT 877

Qy        751 ------------------------------------GTGGATGGGAGCTGGGAAGTGTG 773
                                                  |||||||||||||||||||||||
Db        878 GTCAGTGCAGAAAATAACCTGCACTTCTCTTTGTCCTGTGGATGGGAGCTGGGAAGTGTG 937

Qy        774 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 GAGCGAATGGTCCGTCTGCAGTCCAGAGTGTGAACATTTGCGGATCCGGGAGTGCACAGC 997

Qy        834 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 ACCACCCCCGAGAAATGGGGGCAAATTCTGTGAAGGTCTAAGCCAGGAATCTGAAAACTG 1057

Qy        894 CACAGATGGTCTTTGCATCCTAGATAAAAAACCTCTTCATGAAATAAAACCCCAAAGC-- 951
              |||||||||||||||||||| |    |  | || |||   ||        |  |
Db       1058 CACAGATGGTCTTTGCATCCTAAACTCCACCACCATGCAGGAACCCAAGGTGACTGCCCT 1117

Qy        952 ----------------ATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 995
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Db       1118 TCAGACGCTATGCCAAATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGTGC 1177

Qy        996 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 TGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAGAG 1237

Qy       1056 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 TGACTATGGCGTGGACGTCATTGACTCTTCTGCATTGACAGGTGGCTTCCAGACCTTCAA 1297

Qy       1116 CTTCAAAACAGTCCGTCAAGCCAAGAATATCATGGAACTAATGATACAAGAAAAATCCTT 1175
              ||||||||||||||||||
Db       1298 CTTCAAAACAGTCCGTCAA---------------------------------------- 1316

Qy       1176 TGGTAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1235
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 -GGGAACTCCCTGCTCCTGAATTCTGCCATGCAGCCAGATCTGACAGTGAGCCGGACATA 1375

Qy       1236 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 CAGCGGACCCATCTGTCTGCAGGACCCTCTGGACAAGGAGCTCATGACAGAGTCCTCACT 1435

Qy       1296 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 CTTTAACCCTTTGTCGGACATCAAAGTGAAAGTCCAGAGCTCGTTCATGGTTTCCCTGGG 1495

Qy       1356 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 AGTGTCTGAGAGAGCTGAGTACCACGGCAAGAATCATTCCAGGACTTTTCCCCATGGAAA 1555

Qy       1416 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAACCACAGCTTTAGTACAATGCATCCCAGAAATAAAATGCCCTACATCCAAAATCTGTC 1615

Qy       1476 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 ATCACTCCCCACAAGGACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGGCG 1675

Qy       1536 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 CTTAGTAATGCCAAATACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCCAGAGGA 1735

Qy       1596 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAGCCTCCAGTCAGATGG 1655
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Db       1736 GAATTCTTGGGAGATTTATATGTCCATCAACCAAGGTGAACCCAG------GTCAGATGG 1789

Qy       1656 CTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCAC 1715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1790 CTCTGAGGTGCTCCTGAGTCCTGAAGTCACCTGTGGTCCTCCAGACATGATCGTCACCAC 1849

Qy       1716 TCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCA 1775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1850 TCCCTTTGCATTGACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCA 1909

Qy       1776 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1910 TTTAAAGAAGAGGACACAGCAGGGCAAATGGGAGGAAGTGATGTCAGTGGAAGATGAATC 1969
```

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Qy       1836 TACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGG 1895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1970 TACATCCTGTTACTGCCTTTTGGACCCCTTTGCGTGTCATGTGCTCCTGGACAGCTTTGG 2029

Qy       1896 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 1955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2030 GACCTATGCGCTCACTGGAGAGCCAATCACAGACTGTGCCGTGAAGCAACTGAAGGTGGC 2089

Qy       1956 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2090 GGTTTTTGGCTGCATGTCCTGTAACTCCCTGGATTACAACTTGAGAGTTTACTGTGTGGA 2149

Qy       2016 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2150 CAATACCCCTTGTGCATTTCAGGAAGTGGTTTCAGATGAAAGGCATCAAGGTGGACAGCT 2209

Qy       2076 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2210 CCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACCTTTAGTCTTCAGATTTCTGT 2269

Qy       2136 CCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCC 2195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2270 CCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTCACTGCCTGCCAGGAAGTCCC 2329

Qy       2196 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2330 GTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCACTGTGCCTTCTCCCTGGAGCG 2389

Qy       2256 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2390 TTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGCATTCGGCAGCTCAAAGGCCA 2449

Qy       2316 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2450 TGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGTGAACGAGAAACCATCACTTT 2509

Qy       2376 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2510 CTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGCCCCAAAGCCTTCAAAATTCC 2569

Qy       2436 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2570 CTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACCCCCAATGCCAAAGGCAAGGA 2629

Qy       2496 CTGGCAGATGTTAGCACAGAAAAACAGCATCAAC---AGGAATTTATCTTATTTCGCTAC 2552
             ||||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db       2630 CTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAGGAATTTATCTTATTTCGCTAC 2689

Qy       2553 ACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGG 2612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2690 ACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGG 2749

Qy       2613 TGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTC 2672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2750 TGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAAACTCTC 2809

Qy       2673 AAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACT 2732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2810 AAACATTTCAGAATCCCAGCTTGATGAAGCCGACTTCAACTACAGCAGGCAAAATGGACT 2869

Qy       2733 CTAG 2736
             ||||
Db       2870 CTAG 2873
```

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RESULT 13
ADC77421
ID   ADC77421 standard; DNA; 2661 BP.
XX
AC   ADC77421;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human transmembrane protein INSP017 partial predicted gene sequence.
XX
KW   INSP017; transmembrane protein; netrin receptor family; netrin; axion;
KW   cell migration; axon path-finding; central nervous system;
KW   inflammatory disease; oncology; cardiovascular disease; cytostatic;
KW   antiinflammatory; immunosuppressive; cardiant; anti-HIV; neuroprotective;
KW   nootropic; antiparkinsonian; antidepressant; neuroleptic; osteopathic;
KW   antiarteriosclerotic; nephrotropic; immunomodulator; antidiabetic;
KW   antiinfertility; gene therapy; cell proliferative disorder;
KW   myeloproliferative disorder; autoimmune disorder; inflammatory disorder;
KW   cardiovascular disorder; neurological disorder; psychiatric disorder;
KW   developmental disorder; bone disease; atherosclerosis;
KW   glomerulonephritis; AIDS; HIV infection; metabolic disorder;
KW   pregnancy disorder; birth complication; human; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2661
FT                   /*tag= a
FT                   /product= "Human INSP017 protein"
FT                   /partial
FT                   /note= "No start or stop codon"
XX
PN   WO2003055915-A2.
XX
PD   10-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-GB005856.
XX
PR   21-DEC-2001; 2001GB-00030721.
XX
PA   (ARES-) ARES TRADING SA.
XX
PI   Fitzgerald SN,  Fagan RJ,  Phelps CB,  Power C,  Yorke M;
XX
DR   WPI; 2003-559270/52.
DR   P-PSDB; ADC77422.
XX
PT   New polypeptide, useful for the manufacture of a medicament for treating
PT   disease, e.g., cell proliferative, autoimmune, inflammatory,
PT   cardiovascular or neurological disorders.
XX
PS   Claim 9; SEQ ID NO 31; 96pp; English.
XX
CC   This invention relates to a novel human protein (INSP017), a
CC   transmembrane protein of the netrin receptor family, and to the use of
CC   this protein and the DNA sequence which encodes it for diagnosis,
CC   prevention and treatment of disease. Netrins are a family of secreted
CC   proteins which are involved in both repelling and attracting axions and
CC   thus function as guidance molecules for cell migration and axon path-
CC   finding processes in the central nervous system. Transmembrane proteins
CC   such as that of the invention have been shown to play a role in diverse
CC   physiological functions and they may be involved in many diseases,
CC   particularly inflammatory diseases, oncology and cardiovascular disease.
CC   Compounds which modulate the transmembrane protein of the invention may
CC   therefore have cytostatic, antiinflammatory, immunosuppressive, cardiant,
CC   anti-HIV, neuroprotective, nootropic, antiparkinsonian, antidepressant,
CC   neuroleptic, osteopathic, antiarteriosclerotic, nephrotropic,
CC   immunomodulator, antidiabetic or antiinfertility activity. In addition,
CC   the protein and amino acid sequence of the invention may be useful for
CC   gene therapy. The protein, nucleic acid (and compound and pharmaceutical
CC   composition) of the invention may be useful for the manufacture of a
CC   medicament for treating disease, such as cell proliferative disorders,
CC   myeloproliferative disorders, autoimmune/inflammatory disorders,
CC   cardiovascular disorders, neurological disorders, psychiatric disorders,
CC   developmental disorders, bone disease, atherosclerosis,
CC   glomerulonephritis, AIDS, HIV infections, metabolic disorders, pregnancy
CC   disorders and birth complications. The present sequence is the partial
CC   predicted DNA sequence of the gene which encodes the protein INSP017 of
CC   the invention.
XX
SQ   Sequence 2661 BP; 680 A; 693 C; 670 G; 618 T; 0 U; 0 Other;
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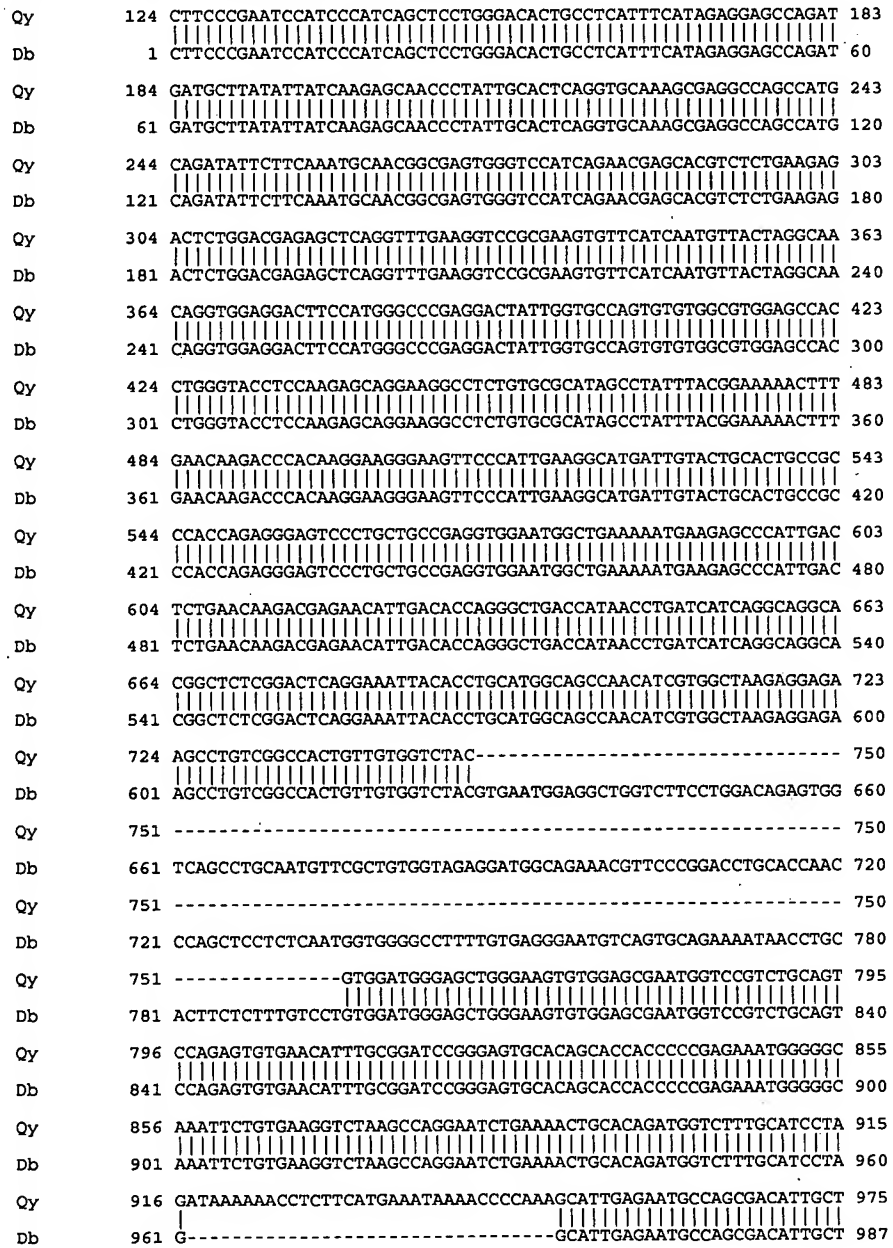
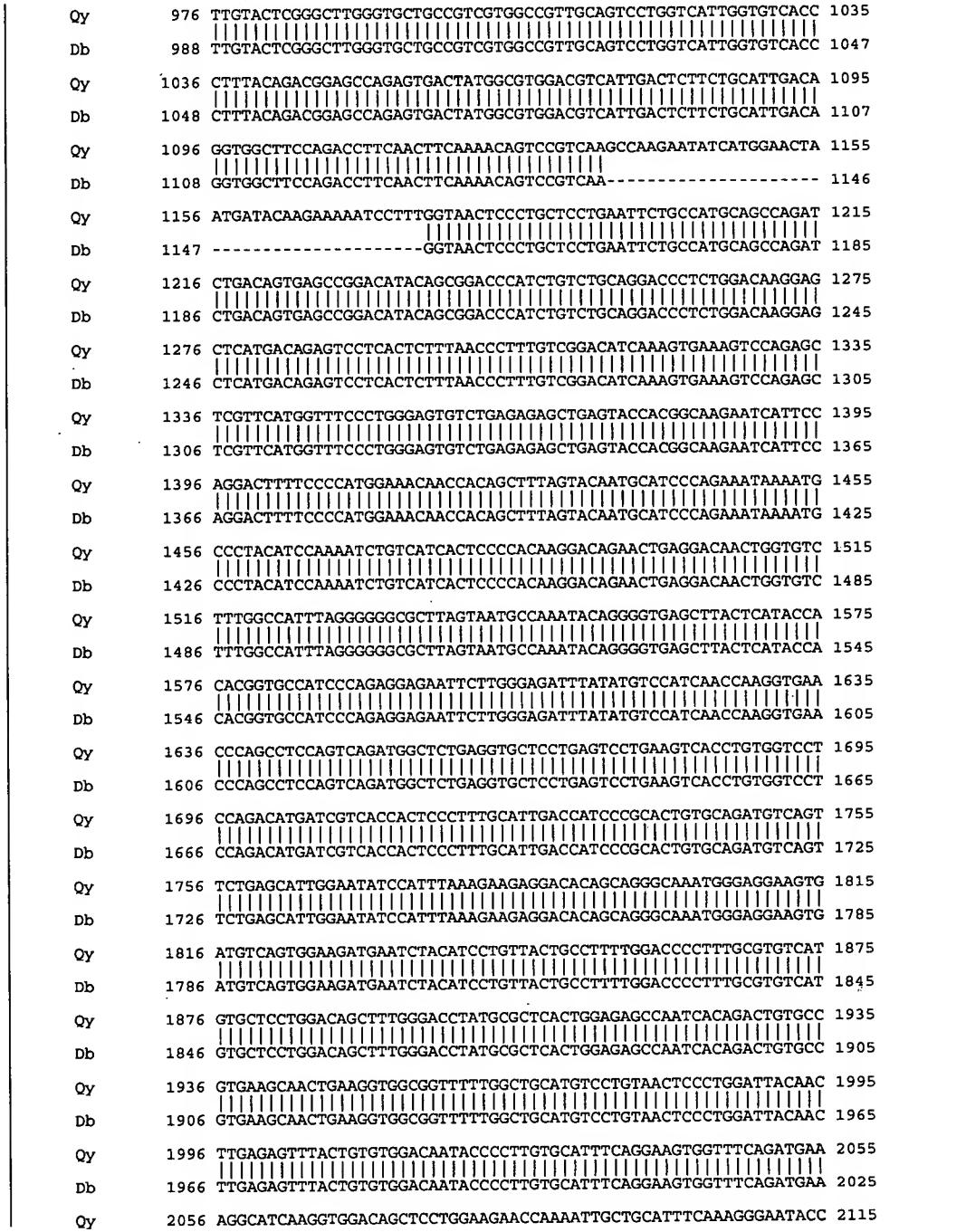
Query Match 81.1%; Score 2220; DB 10; Length 2661;
Best Local Similarity 91.1%; Pred. No. 0;
Matches 2493; Conservative 0; Mismatches 0; Indels 243; Gaps 3;





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Db       2026 AGGCATCAAGGTGGACAGCTCCTGGAAGAACCAAAATTGCTGCATTTCAAAGGGAATACC 2085

Qy       2116 TTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTC 2175
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 TTTAGTCTTCAGATTTCTGTCCTTGATATTCCCCCATTCCTCTGGAGAATTAAACCATTC 2145

Qy       2176 ACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCAC 2235
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 ACTGCCTGCCAGGAAGTCCCGTTCTCCCGCGTGTGGTGCAGTAACCGGCAGCCCCTGCAC 2205

Qy       2236 TGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGC 2295
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Db       2206 TGTGCCTTCTCCCTGGAGCGTTATACGCCCACTACCACCCAGCTGTCCTGCAAAATCTGC 2265

Qy       2296 ATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGT 2355
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Db       2266 ATTCGGCAGCTCAAAGGCCATGAACAGATCCTCCAAGTGCAGACATCAATCCTAGAGAGT 2325

Qy       2356 GAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGC 2415
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 GAACGAGAAACCATCACTTTCTTCGCACAAGAGGACAGCACTTTCCCTGCACAGACTGGC 2385

Qy       2416 CCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACC 2475
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 CCCAAAGCCTTCAAAATTCCCTACTCCATCAGACAGCGGATTTGTGCTACATTTGATACC 2445

Qy       2476 CCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAAT 2535
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 CCCAATGCCAAAGGCAAGGACTGGCAGATGTTAGCACAGAAAAACAGCATCAACAGGAAT 2505

Qy       2536 TTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCT 2595
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 TTATCTTATTTCGCTACACAAAGTAGCCCATCTGCTGTCATTTTGAACCTGTGGGAAGCT 2565

Qy       2596 CGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGG 2655
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 CGTCATCAGCATGATGGTGATCTTGACTCCCTGGCCTGTGCCCTTGAAGAGATTGGGAGG 2625

Qy       2656 ACACACACGAAACTCTCAAACATTTCAGAATCCCAG 2691
                |||||||||||||||||||||||||||||||||||
Db       2626 ACACACACGAAACTCTCAAACATTTCAGAATCCCAG 2661


RESULT 14
ADR44602
ID   ADR44602 standard; cDNA; 2043 BP.
XX
AC   ADR44602;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Novel human protein (NHP) encoding cDNA #13.
XX
KW   Novel human protein; NHP; drug screening; clinical trial monitoring;
KW   cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW   gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2043
FT                   /*tag=  a
FT                   /product= "Novel human protein (NHP)"
FT   variation       replace(83,C)
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
FT   variation       replace(95,C)
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
FT   variation       replace(583,T)
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   US6777232-B1.
XX
PD   17-AUG-2004.
XX
PF   02-OCT-2001; 2001US-00969532.
XX
PR   02-OCT-2000; 2000US-0237280P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Scoville J;
XX
DR   WPI; 2004-591302/57.
DR   P-PSDB; ADR44603.
XX
PT   New isolated human proteins and nucleic acids, useful for diagnosing,
PT   drug screening, clinical trial monitoring, or treating diseases and
PT   disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS   Disclosure; SEQ ID NO 25; 52pp; English.
XX
CC   The present invention provides novel human proteins (NHPs) and their
CC   encoding polynucleotides. The invention is useful for diagnosis, drug
CC   screening, clinical trial monitoring, treatment of diseases and disorders
CC   such as cancer and arthritis and cosmetic applications. The invention
CC   acts as a cytostatic and virucidal agent. The invention is useful in gene
CC   therapy. The present sequence is a novel human protein (NHP) encoding
CC   cDNA. The NHP encoding cDNA is located on human chromosome 8.
XX
SQ   Sequence 2043 BP; 541 A; 531 C; 485 G; 486 T; 0 U; 0 Other;

  Query Match             74.7%;  Score 2043;  DB 13;  Length 2043;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2043;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        694 ATGGCAGCCAACATCGTGGCTAAGAGGAGAAGCCTGTCGGCCACTGTTGTGGTCTACGTG 753
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Db        241 GAAATAAAACCCCAAAGCATTGAGAATGCCAGCGACATTGCTTTGTACTCGGGCTTGGGT 300

Qy        994 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 1053
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGCCGTCGTGGCCGTTGCAGTCCTGGTCATTGGTGTCACCCTTTACAGACGGAGCCAG 360

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RESULT 15
ADR44604
ID ADR44604 standard; cDNA; 2010 BP.
XX
AC ADR44604;
XX
DT 04-NOV-2004 (first entry)
XX
DE Novel human protein (NHP) encoding cDNA #14.
XX
KW Novel human protein; NHP; drug screening; clinical trial monitoring;
KW cancer; arthritis; cosmetic application; cytostatic; virucidal;
KW gene therapy; human; SNP; single nucleotide polymorphism; chromosome 8;
KW gene; ss.
XX
OS Homo sapiens.
XX

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FT	variation	replace(550,T)
FT		/*tag= d
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PN US6777232-B1.
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PD 17-AUG-2004.
XX
PF 02-OCT-2001; 2001US-00969532.
XX
PR 02-OCT-2000; 2000US-0237280P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX

PI Walke DW, Scoville J;
XX
DR WPI; 2004-591302/57.
DR P-PSDB; ADR44605.
XX
PT New isolated human proteins and nucleic acids, useful for diagnosing,
PT drug screening, clinical trial monitoring, or treating diseases and
PT disorders, e.g. treating cancer, arthritis, or as antiviral agents.
XX
PS Disclosure; SEQ ID NO 27; 52pp; English.
XX
CC The present invention provides novel human proteins (NHPs) and their
CC encoding polynucleotides. The invention is useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and disorders
CC such as cancer and arthritis and cosmetic applications. The invention
CC acts as a cytostatic and virucidal agent. The invention is useful in gene
CC therapy. The present sequence is a novel human protein (NHP) encoding
CC cDNA. The NHP encoding cDNA is located on human chromosome 8.
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SQ Sequence 2010 BP; 523 A; 523 C; 484 G; 480 T; 0 U; 0 Other;

Query Match 71.9%; Score 1967; DB 13; Length 2010;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2010; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy       2734 TAG 2736
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Search completed: April 1, 2005, 05:38:18
Job time : 1388 secs